

1 **Supporting Information**

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3 **A cold shock protein promotes high-temperature microbial growth
4 through binding to diverse RNA species**

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24 **Keywords:** heat shock response, global RNA chaperone, CspL, mRNA binding

25

26 **SI Materials and Methods**

27

28 **Bacterial growth conditions and quantification of cell density**

29 To evaluate the growth of *Bacillus coagulans* 2-6 under different temperatures, cells were
30 grown overnight in 100 ml of GSY medium (20 g/l glucose, 10 g/l yeast extract, 5 g/l tryptone,
31 5 g/l CaCO₃) without antibiotics in 250 ml Erlenmeyer flasks at 37 °C and 60 °C on a rotary
32 shaker (200 rpm). *E. coli* and *Pseudomonas putida* were grown in Luria-Bertani (LB) medium
33 with appropriate antibiotics at 37 °C, and *Saccharomyces cerevisiae* was grown in yeast
34 extract peptone dextrose medium (YEPD medium: 10 g/l yeast extract, 10 g/l peptone, 20 g/l
35 glucose) with appropriate antibiotics at 37 °C. Cell densities were monitored by measuring
36 optical density at 600 nm using a MAPADA V-1200 spectrophotometer. The overnight
37 cultures were used to seed fresh medium (OD₆₀₀ of 0.1 at the time of transfer). Growth at
38 37 °C and 60 °C was monitored every 2 hours throughout the incubation period. For dry cell
39 weight measurements, a 30 ml cell suspension was centrifuged at 12,000 g for 8 min in pre-
40 weighed microcentrifuge tubes. The cell pellets were washed twice in water and dried at
41 50 °C until the mass of each tube remained constant over time (typically after ~48 h).

42

43 **Preparation of proteomes, 2D-LC/MS analysis, and protein identification**

44 Cells of *B. coagulans* 2-6 grown in GSY medium were harvested by centrifugation, washed
45 twice in PBS buffer, and the cell pellets were lysed by resuspending in buffer (8 M urea,
46 0.05% SDS, 10 mM DTT, 10 mM Tris, pH 8.0) and grinding under liquid nitrogen. After
47 centrifugation at 12,000 g (10 min, 4 °C), the supernatant was mixed with precooled acetone
48 at a volume-to-volume ratio of 1:4. Following overnight incubation at -20 °C, the mixture was
49 centrifuged at 12,000 g (10 min, 4 °C). The pellets were washed with precooled acetone three
50 times, and resuspended in buffer containing 6 M Gu-HCl and 100 mM Tris, pH 8.3. The
51 protein content was measured using a modified Bradford protocol. Total protein (100 µg) was
52 resuspended in buffer containing 10 mM DTT and incubated at 56 °C for 0.5 h. Then 50 mM
53 IAA was added, and the sample was incubated at 25 °C for 40 min. After 3 K ultrafiltration,
54 membrane ultrafiltration, and flushing of the membrane with 100 mM NH₄HCO₃, the pH of
55 the solution was adjusted to 8.0-8.5. Next, 40 µg of sequencing-grade modified trypsin was
56 added to the extract and digestion was carried out overnight at 37 °C with gentle rotation
57 (protein : trypsin ratio = 50 : 1).

58 In order to separate and analyze the peptides in the samples, we used multi-dimensional
59 liquid chromatography with an Agilent 1100 LC system. Separation in the first dimension

60 began with the elution of peptides from a strong cation exchange silica column (0.075 mm × 5
61 cm). Next, a C18 column (0.075 mm × 10 cm) (Column Technology Inc.) was used with a
62 continuous linear salt gradient (0 - 130 min, 2% - 35%; 130 - 135 min, 35% - 90%; 135 - 140
63 min, 90%; 140 - 141 min, 90% - 2%; 141 - 180 min, 2%); Chromatography conditions: buffer
64 A: H₂O; buffer B: acetonitrile. Finally, a nanospray column was directly interfaced to the
65 orifice of an LTQ Classic ion trap mass spectrometer (ThermoFisher). Nanospray ionization
66 was accomplished with a spray voltage of 3.5 kV and capillary temperature of 200 °C. The
67 m/z scan range was from 400 to 1800.

68 Database searches for MS and MS/MS spectra were conducted using proteomics
69 discovery software V1.2 (ThermoFisher, CA, USA). Mass spectra were analyzed using
70 Bioworks software. We generated a predicted protein database from the annotated *B.*
71 *coagulans* 2-6 genome. The peptide matches with an assumed charge state of z = 1 and an
72 XCorr score of > 2.2, or charge state of z = 3 and an XCorr score of > 3.75 were
73 automatically accepted as valid. High scoring peptide matches were automatically identified
74 and retained.

75

76 **RNA deep-sequencing and identification of differentially expressed mRNA**

77 Total RNA was extracted from *B. coagulans* 2-6 and *E. coli* DH5α with the RNAiso Plus kit
78 (Takara, Japan). RNA deep-sequencing was performed by a commercial sequencing company
79 (Novogene, China). Briefly, sequencing libraries were generated from rRNA-depleted RNA
80 using the NEBNext® Ultra™ Directional RNA Library Prep Kit for Illumina® (NEB, USA)
81 following the manufacturer's recommendations. The libraries were sequenced on the Illumina
82 Hiseq 2000 platform, and 100 bp paired-end reads were generated. Demultiplexed and quality
83 filtered reads were then aligned to *B. coagulans* 2-6 and *E. coli* DH5α reference genome
84 sequence using TopHat (V.2.0.8). The mapped reads from each sample were assembled using
85 Trinity with a reference-based approach.

86 Cuffdiff (v2.1.1) was used to calculate the RPKM (Reads Per Kilobase per Million
87 mapped reads) of coding genes in each sample. Gene RPKM values were computed by
88 summing the FPKM values of transcripts in each gene group. Cuffdiff provides a statistical
89 method for determining differential expression of digital transcripts or gene expression data
90 using a model based on the negative binomial distribution. Genes with a P value < 0.05,
91 FKPRM > 0.5 and FC > 2 were classified as differentially expressed.

92

93 **Expressing *B. coagulans* 2-6 genes in *E. coli*, *S. cerevisiae*, and *P. putida***

94 PCR amplification was carried using the Phanta Super-Fidelity DNA Polymerase (Vazyme,
95 China) according to the manufacturer's instructions. The sequences of all the plasmids
96 produced were verified by restriction mapping and/or DNA sequencing. We cloned 38 genes
97 from *B. coagulans* 2-6 (*Supplementary Table S5*) into the pUC19 vector and then transformed
98 these constructs into *E. coli* DH5 α competent cells. Positive transformants were selected on
99 LB medium plates containing ampicillin (50 mg/l) and were confirmed via PCR. We also
100 cloned the *BCO26_cspL* gene into the pYES2 and pME6032 vectors and then transformed
101 these constructs into *S. cerevisiae* and *P. putida* competent cells, respectively. Positive *S.*
102 *cerevisiae* and *P. putida* transformants were selected on YPD medium containing 50 mg/l
103 ampicillin and LB medium containing 25 mg/l tetracycline, respectively, and were confirmed
104 via PCR.

105 The growth of the transformants at 37 °C and 45 °C was monitored via absorbance
106 measurements using a Bioscreen C® analyzer (Labsystems, Finland). All transformants were
107 grown overnight at 42 °C and then inoculated into fresh media in Honeycomb plates (10 × 10
108 wells) containing the appropriate antibiotics. Quintuplicates of each engineered strain were
109 aliquoted into 200 μ l wells. The plates were shaken continuously; readings were taken at a
110 wavelength of 600 nm.

111

112 **Bio-Layer Interferometry (BLI)**

113 Octet RED96 System (ForteBio) was used for BLI studies. Assay was performed in black 96
114 well plates (NuncF96 MicroWell TM Plates, Thermo Fisher Scientific, Langenselbold,
115 Germany). The total working volume for samples or buffer was 0.2 ml per well. All binding
116 studies were carried out at 25 °C. Prior each assay, streptavidin (SA) biosensor tips (ForteBio)
117 were pre-wetted in 0.2 ml PBS for at least 20 min. In the preparation stage, sequences
118 synthesized by using 5'-biotin modification (sequences are presented in Supplementary Table
119 S10). SA sensors were loaded with biotinylated single strand RNA/DNA (10 μ M), in a buffer
120 containing 20 mM PBS, pH 7.4, 100 mM NaCl, 0.1% BSA (w/v) and 0.02% Tween 20 (v/v).
121 After reaching base line in the same buffer, association and dissociation were carried out with
122 purified CspL (20 μ g/ml) and buffer respectively. Steady-state binding responses were
123 determined by the overall response (nm) on each sensor sensor. All measurements were
124 performed in triplicates. The association and dissociation responses were baseline corrected
125 processed with the Octet Software (Version 7.0, ForteBio). Interferometry data were globally
126 fit to a simple 1 : 1 Langmuir model calculating the affinities and rate constants (Octet
127 Software, Version 7.0, ForteBio). The association rate constant (k_a) is defined as the rate of

128 complex formation per second in a 1 molar solution of two reaction partners. The dissociation
129 rate constant (k_d) indicates the stability of this complex. The affinity constant K_D is calculated
130 by the ratio of the k_d/k_a .

131

132 **RIP-seq experiment**

133 Cells were cultured overnight in LB medium with ampicillin. After centrifugation the
134 supernatant was discarded, and the pellet was washed twice with 5 ml of ice-cold PBS and
135 lysed with 600 μ l of lysis buffer (20 mM Tris-HCl pH 7.4, 150 mM NaCl, 5 mM MgCl₂,
136 and 1 mM DTT) containing 1% Triton X-100 and Turbo DNase I (Invitrogen) 25 U/ml. The
137 sample was then clarified by centrifugation for 10 min at 20,000 g, 4 °C. The supernatant was
138 incubated at 4 °C for 30 min with 60 μ l of Dynabeads M-270 Streptavidin (Invitrogen)
139 equilibrated with lysis buffer containing 1% Triton X-100. The beads were washed three
140 times with lysis buffer containing 1% Triton X-100 and 1 M NaCl. His-BCO26-CspL and
141 bound RNAs were eluted with 25 μ l of lysis buffer containing 5 mM biotin at 4 °C for 30
142 min. RNAs were extracted with QIAzol (Qiagen) using the Direct-zol RNA miniprep (Zymo
143 Research). Sequencing libraries were prepared using the TruSeq Stranded Total RNA Library
144 Prep Kit with Ribo-Zero Gold (Illumina). Libraries were sequenced on the HiSeq2500
145 (Illumina) platform.

146

147 **mRNA level assay**

148 *E. coli* overnight cultures were diluted 1:100 into 25 ml fresh LB media and incubated at
149 37 °C or 45 °C until reaching an optical density (OD₆₀₀) of 0.5. The culture was then placed in
150 a preheated 37 °C shallow water bath to preserve the experiment temperature and 125 μ l
151 Rifampicin (100 mg/ml, for a final concentration of 500 μ g/ml) were immediately added to
152 the culture to inhibit RNA synthesis. After rifampicin treatment, rifampicin was removed and
153 put the samples back into the incubators. Selected time points were sampled by collecting 1.4
154 ml from the culture into a pre-chilled tube containing 170 μ l of ice-cold stop solution (90%
155 ethanol and 10% saturated phenol) to deactivate cellular processes and RNA-decay. The
156 sample was quickly vortexed and then extracted total RNA by using RNA Easy Fast Kit
157 (TIANGEN, DP451).

158

159 **Validating the function of CspL in *E. coli* eGFP expressing system, *Actinosynnema* 160 *pretiosum*, and *Bacillus licheniformis* fermentation**

161 For validating the function of CspL, *E. coli* eGFP expressing system (strain *E. coli* eGFP) was
162 constructed. The gene sequence of eGFP (Pfam: 01353) was synthesized by Sangon
163 (Shanghai) and transferred into *E. coli* DH5 α competent cell by harboring plasmid pET28a.
164 Using LB plate and PCR to confirm positive transformants, the plasmid pUC19 harboring
165 *cspL* was then transferred into those competent positive transformants, and confirmed via
166 PCR. The control group used empty pUC19 vector in place of pUC19-*cspL*. Wild type,
167 control, and *E. coli* eGFP-pUC19-*cspL* were grown overnight in LB medium at 45 °C. The
168 overnight culture was inoculated 1 : 100 into fresh LB medium with appropriate antibiotic (20
169 μ g/ml kanamycin and 100 μ g/ml ampicillin) to create a culture stock. The 250 ml Erlenmeyer
170 flasks contained 50 ml of culture stock and cultured in the shaker at 45 °C. Every two hours,
171 the cultures were checked for cell density and fluorescence signal. The method of cell density
172 was mentioned previously. An aliquot of the fresh culture stock (200 μ l) was transferred into
173 polystyrene 96-well Costar Assay Plate (black with clear flat bottom, Corning Inc., New
174 York). The plate was shaken in linear mode for 30 s and green fluorescence ($\lambda_{ex} = 485$ nm,
175 $\lambda_{em} = 535$ nm) was monitored using an Infinite F200 multimode reader (TECAN, San Jose,
176 CA).

177 For evaluating the function of CspL in high value-added industrial microbes, *A. pretiosum*
178 ATCC31280 (used as AP-3 producing strain) and its derivatives were cultured at 30 °C on
179 YMG agar (0.4% yeast extract, 1.0% malt extract, 0.4% glucose, 2.0% agar (w/v), pH 7.2-
180 7.3). For metabolites analysis, the first seed medium (3.0% tryptone soya broth powder, 0.5%
181 yeast extract and 5.0% sucrose (w/v), pH 7.5) was inoculated with agar-grown mycelia and
182 cultivated at 30 °C, 220 rpm for 24h. Subsequently, the second medium (3.0% tryptone soya
183 broth powder, 0.5% yeast extract and 2.5% sucrose, 1.0% soluble starch (w/v), 0.05%
184 isobutanol and 0.05% isopropanol (v/v), pH 7.5) was inoculated with 1 ml of the first seed
185 culture, inoculated for another 24 h at 30 °C. Fermentation medium (yeast extract 0.8%, malt
186 extract 1.0%, sucrose 1.5%, soluble starch 2.5% (w/v), isobutanol 0.5%, isopropanol 1.2%
187 (v/v), pH 7.5) was inoculated with the second seed culture at 10% (v/v) and inoculated at
188 25 °C and 220 rpm for 7 days. *E. coli* DH10B and *E. coli* ET12567/pUZ8002 were used for
189 plasmid construction and intergeneric conjugation, respectively. For overexpression of the
190 gene *cspL*, the plasmid pLQ856 with the kasOp* promoter cloned into BamHI/SpeI-digested
191 plasmid pDR3 was used. The sequenced *cspL* encoding gene was inserted into plasmid
192 pLQ856 under the control of kasOp* promoter, generating plasmid pLQ856-*cspL*. The
193 recombinant plasmid was introduced into ATCC31280 from *E. coli* ET12567/pUZ8002
194 through intergeneric conjugation. Additionally, the plasmid pLQ856 was introduced into

195 ATCC31280 generating a control strain ATCC31280::pLQ856. To quantify AP-3 production,
196 the supernatant of the fermentation broth was extracted with 2 volume of ethyl acetate and
197 evaporated. The residues were dissolved in methanol, passed through 0.22- μ m filters, and
198 applied to HPLC. The HPLC analysis was operated on Agilent series 1260 (Agilent
199 Technology, USA) with an Agilent Eclipse Plus-C18 column (4.6 \times 150 mm, 5 μ m). AP-3
200 analyzed at a flow rate of 0.5 ml/min, with the following gradient: 0-5 min 10%-50% B, 5-10
201 min 50%-60% B, 10-20 min 60%-75% B, 20-30 min 75%-95% B, 30-38 min 95% B, 38-39
202 min 95%-10% B, 39-48 min 10% B (solvent A: water, solvent B: methanol), and detected at
203 236 nm and 254 nm.

204 The synthetic DNA fragment with the inducible promoter Pgrac100 and the codon-
205 optimized gene *cspL* was ligated into the *E. coli*-*B. subtilis* shuttle vector pEB03 to generate
206 the plasmid pEB03-Pgrac100*cspL*. The plasmid pEB03-Pgrac100*cspL* and pEB03 were
207 transformed into *B. licheniformis* BN11 using the method as described previously. *B.*
208 *licheniformis* were statically cultivated in GSY medium at 50 °C for 24 h. The D-lactate
209 fermentation medium is composed of 100 g/l glucose, 40 g/l peanut meal 0.3 g/l neutral
210 protease. The fermentation temperature was controlled at 50 °C and the inoculum volume was
211 10% (v/v). The pH was maintained at 7.0 by the automated addition of 25% (w/v) Ca(OH)₂.
212 The glucose concentration was maintained between 20 g/l and 120 g/l by adding glucose
213 powder. After 10 h of fermentation, 0.1 mM IPTG was added. Glucose concentration was
214 estimated by the SBA-40D biosensor analyzer. Lactate concentration was determined by
215 HPLC using a Bio-Rad Aminex HPX-87H column.
216

217 **Nano-HPLC-MS/MS analysis for CspL expression**

218 Lysis buffer (1% SDS, 7 M urea, 1x Protease Inhibitor Cocktail (Roche Ltd. Basel,
219 Switzerland)) was added into the samples, which were vibrated and milled for 400 s three
220 times. The samples were then lysed on ice for 30 min and centrifuged at 15,000 rpm for
221 15min at 4 °C. The supernatant was collected and transferred to a new Eppendorf tube. A total
222 of 100 μ g of protein per condition was transferred into a new Eppendorf tube and the final
223 volume was adjusted to 100 μ L with 8 M urea. TCEP (2 μ L of 0.5 M) was added and the
224 sample was incubated at 37 °C for 1 h, and then 4 μ L of 1 M iodoacetamide was added to the
225 sample and the incubated for 40 minutes at room temperature and protected from light. After
226 that, five volumes of -20 °C pre-chilled acetone were added to precipitate the proteins
227 overnight at -20 °C. The precipitates were washed twice using 1 mL pre-chilled 90% acetone
228 aqueous solution and then re-dissolved in 100 μ L 100 mM TEAB. Sequence grade modified

229 trypsin (Promega, Madison, WI) was added at the ratio of 1:50 (enzyme: protein, weight :
230 weight) to digest the proteins at 37 °C overnight. The peptide mixture was desalted by C18
231 ZipTip and then lyophilized using a SpeedVac. The sample was analyzed by on-line
232 nanospray LC-MS/MS on Orbitrap Fusion™ Lumos™ Tribrid™ mass spectrometer (Thermo
233 Fisher Scientific, MA, USA) coupled to an EASY-nanoLC 1000 system (Thermo Fisher
234 Scientific, MA, USA). A total of 2 µL peptide was loaded (analytical column: Acclaim
235 PepMap C18, 75 µm × 25 cm) and separated with a 60 min gradient. The column flow rate
236 was maintained at 600 nL/min with the column temperature of 40 °C. The electrospray
237 voltage of 2 kV versus the inlet of the mass spectrometer was used. The mass spectrometer
238 was run under data dependent acquisition mode, and automatically switched between MS and
239 MS/MS mode. The parameters were: (1) MS: scan range (m/z) = 350–1500; resolution =
240 120,000; AGC target = 8e5; maximum injection time = 50 ms; include charge states = 2-7; (2)
241 HCD-MS/MS: resolution = 15,000; isolation window = 4; AGC target = 5e4; maximum
242 injection time = 25 ms; collision energy = 25, 30, 35.

243 Tandem mass spectra were processed by PEAKS Studio version X+ (Bioinformatics
244 Solutions Inc., Waterloo, Canada). PEAKS DB was set up to search the
245 uniprot_Escherichia_coli&origin database assuming trypsin as the digestion enzyme. PEAKS
246 DB were searched with a fragment ion mass tolerance of 0.02 Da and a parent ion tolerance of
247 7 ppm. Carbamidomethylation (C) was specified as the fixed modification. Oxidation (M),
248 Deamidation (NQ), QY(X) 314.00, and acetylation (protein N-term) were specified as the
249 variable modifications. The peptides with $-10\lg P \geq 20$ and the proteins with $-10\lg P \geq 20$ and
250 containing at least one unique peptide were filtered.

251

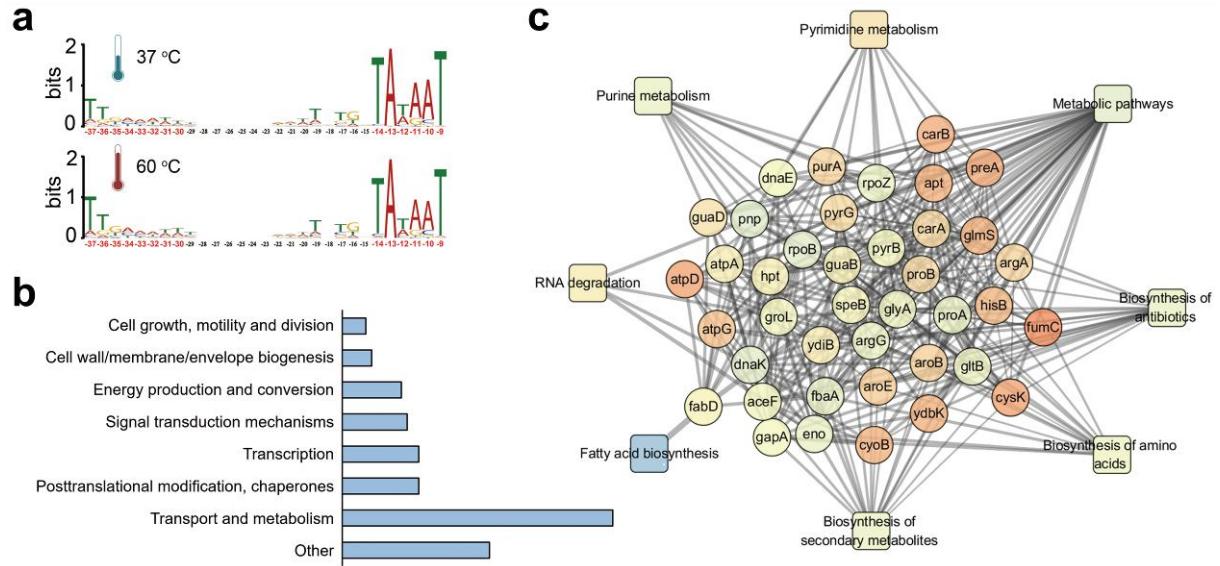
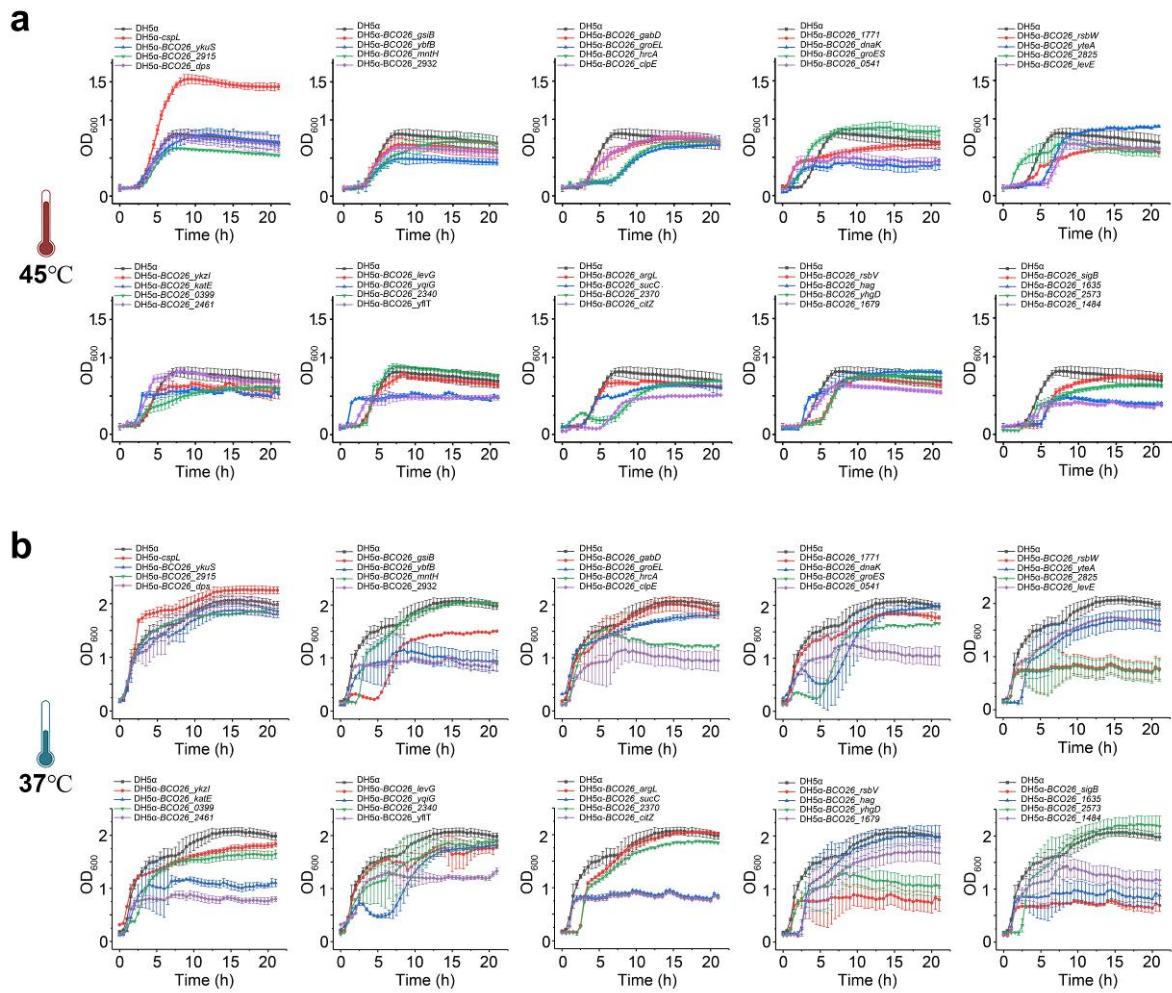


Fig. S1. Transcriptome and proteome analysis of *B. coagulans* 2-6. a Sequence elements of promoters under different conditions. Culturing at 37 °C and 60 °C, the transcriptional start sites, operon structure and the length of 5' UTR does not show significant difference. The regions -14 to -9 and -37 to -30 are highly conservation under different conditions. **b** GO Slim Mapper analysis was performed on the label-free proteome data set to identify the processes of up-regulated protein expressions at 60 °C. **c** Protein-protein interaction network of *B. coagulans* 2-6. Circle node color indicates genetic neighborhood connectivity. Light blue, low; light yellow, medium; light orange, high. Round rectangle nodes color indicates different classification of GO analysis. Under different conditions of *B. coagulans* 2-6, a subset of highly connected protein nodes involved in key cellular processes undergoes temperature fluctuation.

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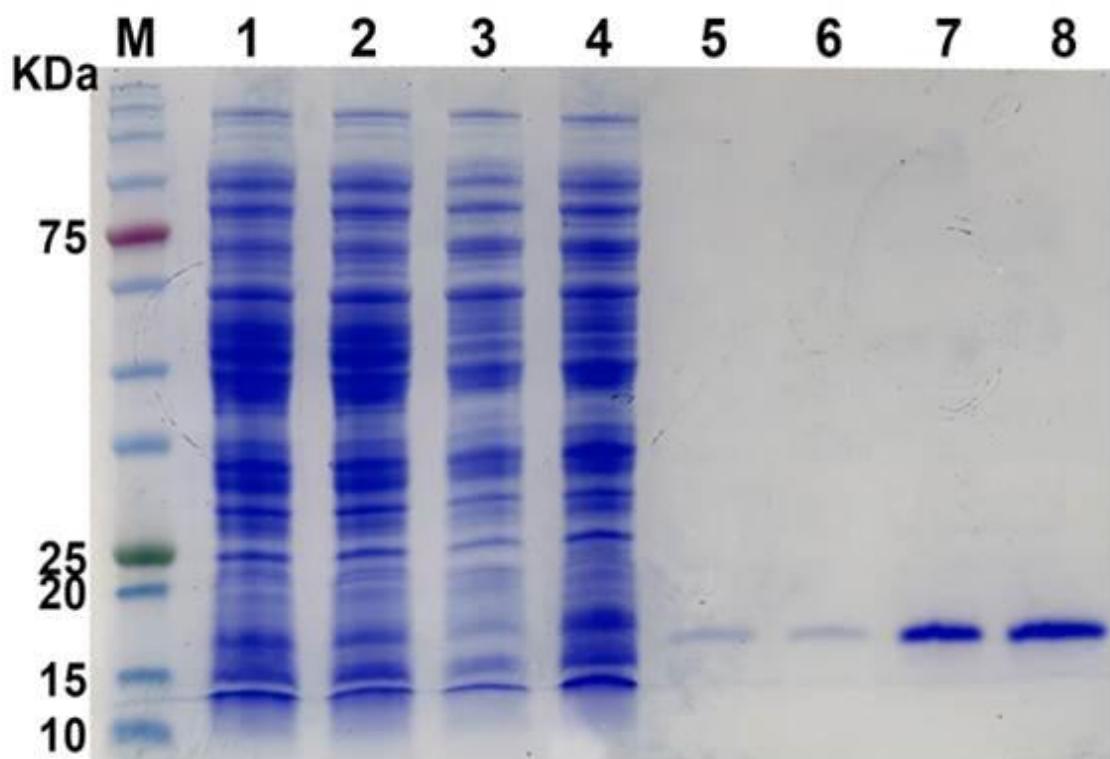
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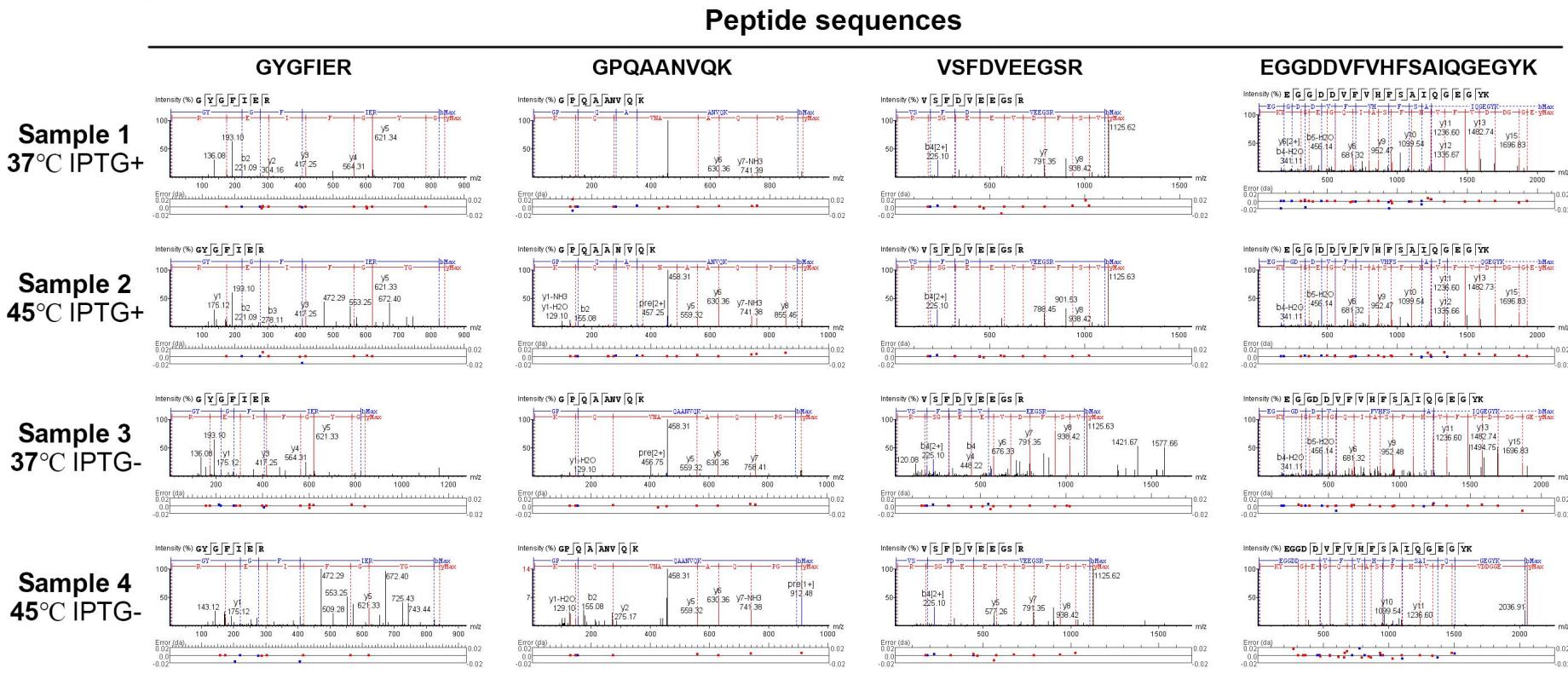
Fig. S2. Growth curves of 38 candidate genes associated with high temperature growth.

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275 **Fig. S3. SDS-PAGE of CspL in *E. coli* DH5 α .** Lane M, marker proteins; Lanes 1 to 4
 276 represent the whole cell lysate samples and Lanes 5 to 8 represent the purification samples of
 277 protein CspL (Ni-NTA affinity, elution by 130 mM imidazole). Lane 1, whole cell lysate,
 278 37 °C, IPTG-; Lane 2, whole cell lysate, 45 °C, IPTG-; Lane 3, whole cell lysate, 37 °C,
 279 IPTG+; Lane 4, whole cell lysate, 45 °C, IPTG+; Lane 5, purified protein CspL, 37 °C, IPTG-;
 280 Lane 6, purified protein CspL, 45 °C, IPTG-; Lane 7, purified protein CspL, 37 °C, IPTG+;
 281 Lane 8, purified protein CspL, 45 °C, IPTG+.

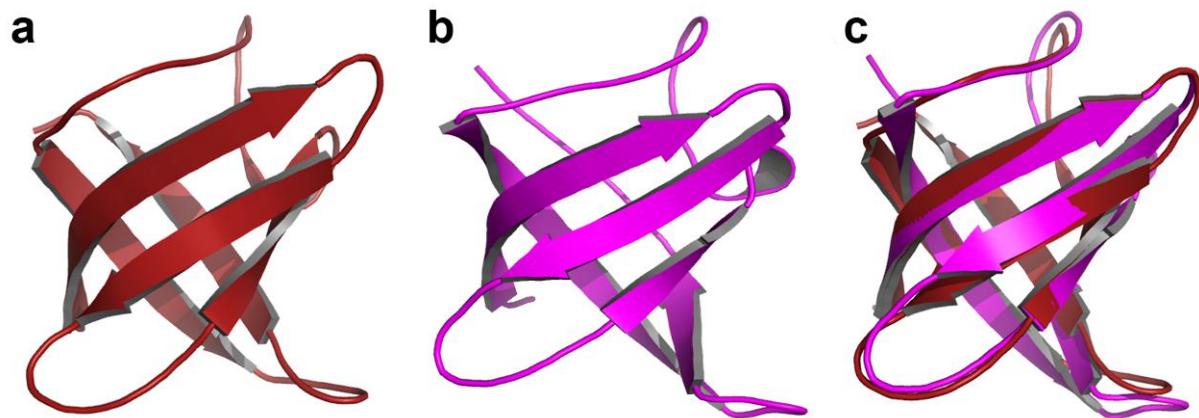


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284 **Fig. S4. CspL peptide identification in nano-HPLC-MS/MS.** The spectrum showed that four unique peptides of target protein were identified by
 285 mass spectrometry under different conditions.

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289 **Fig. S5. The predicted structure of CspL.** **a** The predicted structure of CspL. **b** The
290 structure of *E. coli* CspA (PDB: 1mjc.1). **c** Comparison of the predicted CspL structure with
291 the structure reported for CspA, RMSD: 0.97.

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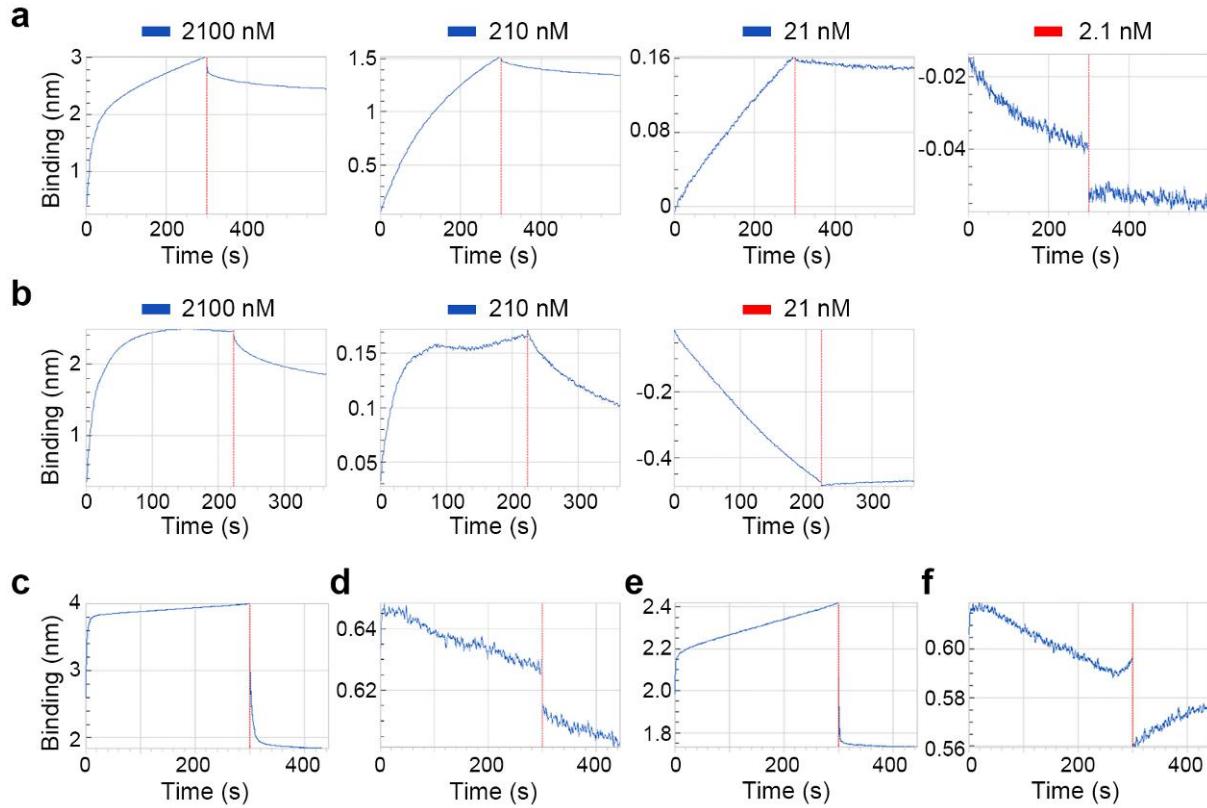
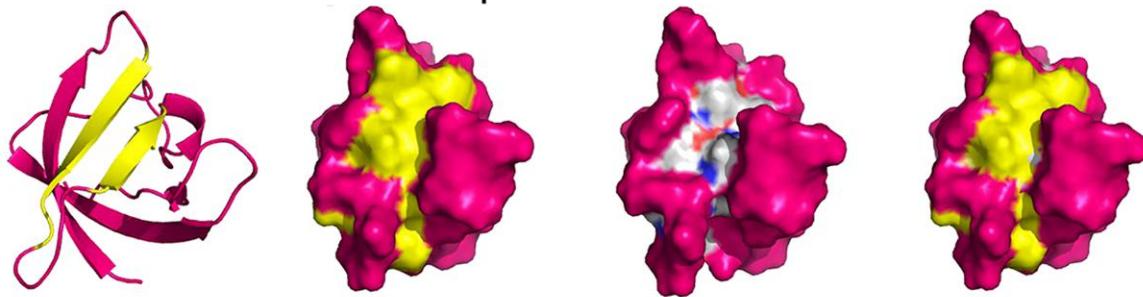
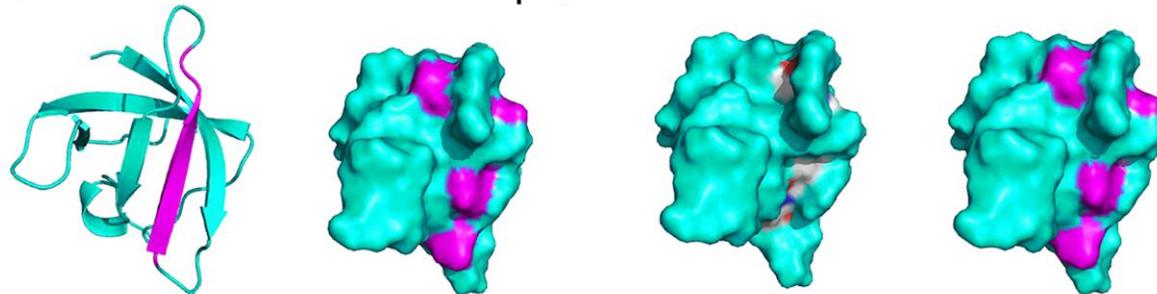


Fig. S6. Concentration limitation of CspL binds to RNA and ssDNA *in vitro*. **a** Concentration limitation of CspL binds to 18 nt RNA fragment. The concentration gradient sets as 2100 nM, 210 nM, 21 nM, and 2.1 nM. When the concentration of CspL set as 2.1 nM, it lost the binding capacity. **b** Concentration limitation of CspL binds to 18 nt ssDNA fragment. The concentration gradient sets as 2100 nM, 210 nM, and 21 nM. When the concentration of CspL set as 21 nM, it lost the binding capacity. **c** Using ssDNA *gaaC* (biotin-CCGCAGAGAACGACGAGAGC) to bind to CspL, it showed positive binding signal. **d** Using complementary double strand of *gaaC* instead of ssDNA, it showed negative binding signal. **e** Using ssDNA random (biotin-CCGCAGATCCAGACGAGAGC) to bind to CspL, it showed positive binding signal. **f** Using complementary double strand of random gene instead of random ssDNA, it showed negative binding signal.

Predicted structure of CspL-M11

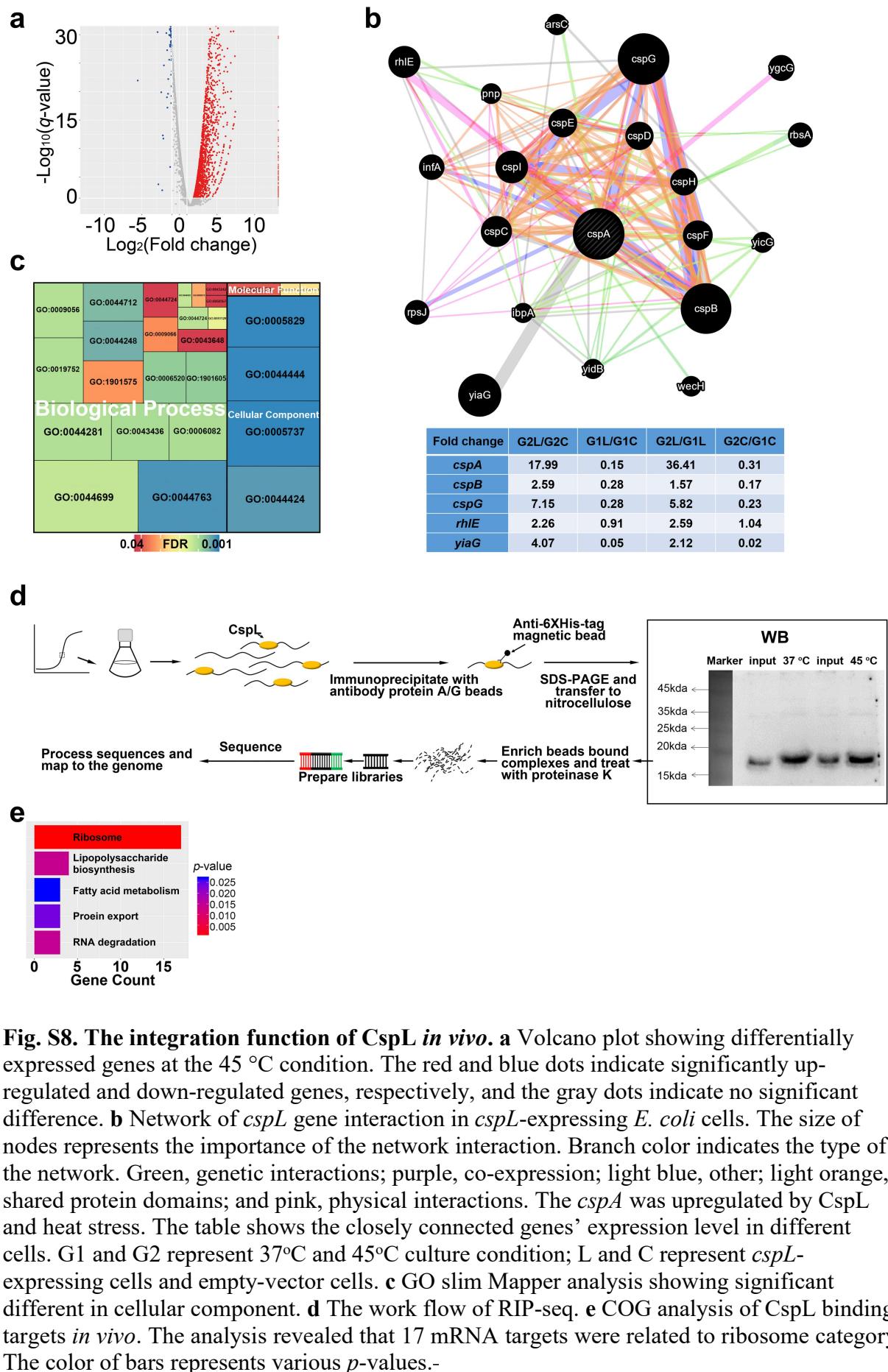


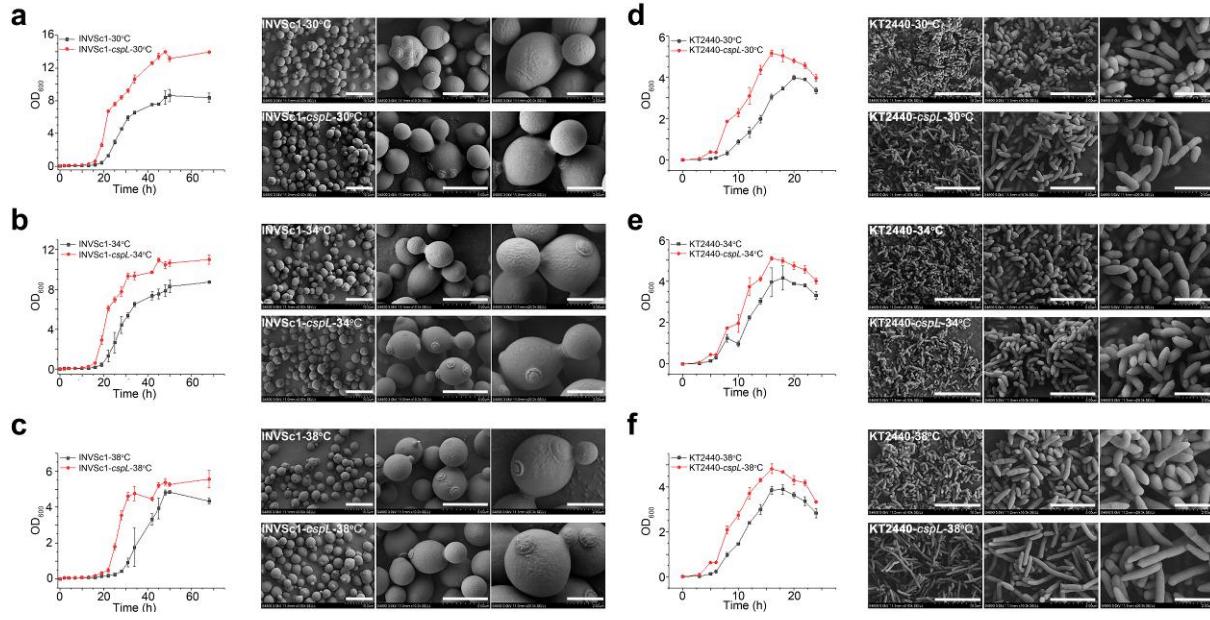
Predicted structure of CspL-M7



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310 **Fig. S7. The mutants of CspL.** Two amino acid mutations were synthesized by a commercial
311 company (Sunny, China). Sequences are listed in Supplementary Table S11. The 11 amino
312 acid mutations predicted structure (row in red). The structure of CspL (hot pink) was
313 predicted and a pair of anti-parallel β -sheets considered as putative ligand-binding domains
314 (yellow) were found. When G14, Y15, G16, F17, I18, E19, R20, V26, F27, V28, and H29 in
315 the putative ligand-binding domain were mutated to Ala (CspL-M11), the area of the ligand-
316 binding domain significantly decreased. The ligand-binding domain mutated is colored in
317 gray. The ligand-binding domain of CspL almost completely covered that of CspL-M11,
318 which further demonstrated the shrink in size of the ligand-binding domain after mutation.
319 The G14, Y15, G16, F17, I18, E19, and R20 in the putative ligand-binding domain mutated to
320 Ala (CspL-M7, colored in blue), which slightly decreased the area of the ligand-binding
321 domain. The ligand-binding domain mutated is colored in gray. The ligand-binding domain of
322 CspL completely covered that of CspL-M7, which further demonstrated the shrink in size of
323 ligand-binding domain after mutation.

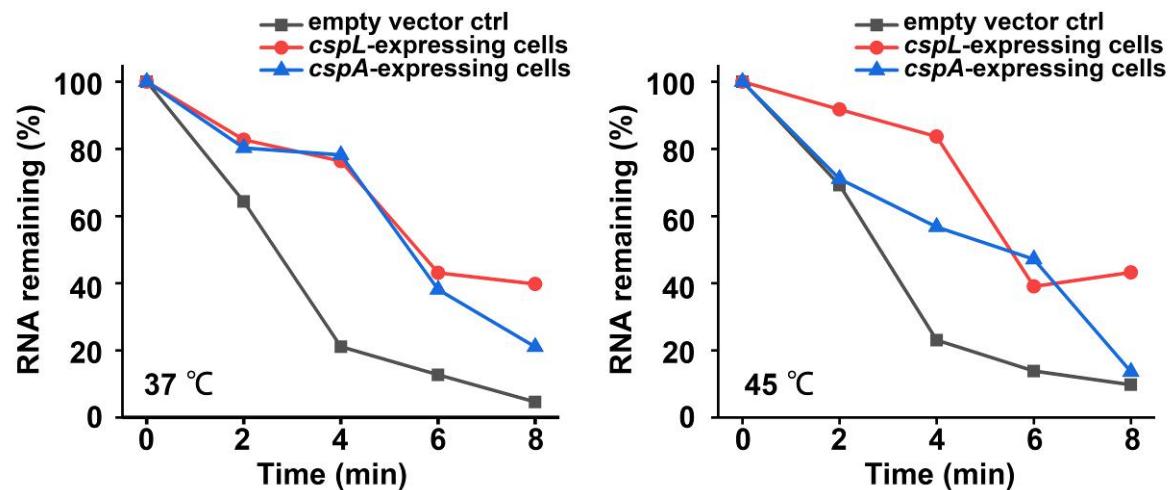


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342 **Fig. S9. Growth curves and SEM images of *S. cerevisiae* and *P. putida* at three**
 343 **temperature gradients at 30 °C, 34 °C, and 38 °C.** In *S. cerevisiae* INVSc1, a, b, and c,
 344 showed CspL expressing grows better than control at different temperature conditions. All
 345 three groups have no significant difference in cell morphology, except, the surface texture of
 346 CspL expressing strain showed obvious smoother than control. In *P. putida* KT2440, d, e, and
 347 f, showed CspL expressing strain grows better than control at different temperature conditions.
 348 Two groups of 30 °C and 34 °C have no significant difference. In 38 °C group, the CspL
 349 expressing strain seemed slightly longer than control. (scare bar from left to right: 10 μm, 5
 350 μm, and 2 μm)

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354

355 Fig. S10. RNA remaining assays. The RNA remaining assays showed CspL and CspA had
 356 the RNA protecting ability compared with empty vector control. Left panel, all samples were
 357 cultured at 37 °C; right panel, samples were cultured at 45 °C.

Supplementary Table 1. Up-regulated genes in *B. coagulans* 2-6 by RNA-seq

Locus	Gene	Log ₂ FC*	Q-value**	Product
BCO26_0715	<i>uvrB</i>	1.3477	0.0488	excinuclease ABC subunit B
BCO26_1892	<i>clpX</i>	1.4211	0.0479	ATP-dependent Clp protease, ATP-binding subunit ClpX
BCO26_2971	<i>trmE</i>	1.4927	0.0289	tRNA modification GTPase TrmE
BCO26_2177	<i>yutG</i>	1.5406	0.0377	phosphatidylglycerophosphatase A
BCO26_1589	<i>resD</i>	1.5476	0.0199	winged helix family two component transcriptional regulator
BCO26_0096	<i>gltX</i>	1.5499	0.0111	glutamyl-tRNA synthetase
BCO26_0306	<i>yqiG</i>	1.6094	0.0296	NADH:flavin oxidoreductase/NADH oxidase
BCO26_2190	<i>sufS</i>	1.6196	0.0230	cysteine desulfurase
BCO26_0964	<i>pdhC</i>	1.6202	0.0363	hypothetical protein
BCO26_2951	<i>rplI</i>	1.6710	0.0290	50S ribosomal protein L9
BCO26_2197	<i>yusI</i>	1.7026	0.0200	arsenate reductase and-like protein
BCO26_1748	<i>hrcA</i>	1.7120	0.0134	heat-inducible transcription repressor HrcA
BCO26_2975	<i>rpmH</i>	1.7207	0.0492	50S ribosomal protein L34
BCO26_0063	<i>folB</i>	1.7284	0.0340	dihydronoopterin aldolase
BCO26_1185	<i>ylxY</i>	1.7293	0.0117	sporulation protein, polysaccharide deacetylase family
BCO26_1352	<i>citB</i>	1.7431	0.0276	aconitate hydratase 1
BCO26_2932	-	1.7449	0.0194	malate/quinone oxidoreductase
BCO26_0951	<i>ykuF</i>	1.7638	0.0302	short-chain dehydrogenase/reductase SDR
BCO26_0090	<i>mcsB</i>	1.7676	0.0036	ATP:guanido phosphotransferase
BCO26_0833	<i>mecA</i>	1.7769	0.0045	Negative regulator of genetic competence
BCO26_1746	<i>dnaK</i>	1.7928	0.0036	chaperone protein DnaK
BCO26_0837	<i>yjbI</i>	1.7956	0.0116	globin
BCO26_1704	<i>pbpA</i>	1.8446	0.0015	penicillin-binding protein transpeptidase
BCO26_2943	<i>yycJ</i>	1.8537	0.0272	beta-lactamase domain-containing protein
BCO26_2952	<i>yybT</i>	1.8883	0.0019	diguanylate cyclase and phosphoesterase
BCO26_0091	<i>clpC</i>	1.8921	0.0019	ATPase AAA-2 domain-containing protein
BCO26_2331	<i>gltD</i>	1.9013	0.0189	glutamate synthase, NADH/NADPH, small

				subunit
BCO26_2036	<i>ytpP</i>	1.9092	0.0200	Thioredoxin domain-containing protein
BCO26_0601	-	1.9444	0.0340	glycoside hydrolase clan GH-D
BCO26_0973	<i>suhB</i>	1.9543	0.0036	inositol monophosphatase
BCO26_0963	<i>pdhB</i>	1.9953	0.0049	transketolase central region
BCO26_0714	-	2.0601	0.0007	hypothetical protein
BCO26_1117	<i>sucC</i>	2.0623	0.0075	succinyl-CoA synthetase subunit beta
BCO26_2480	<i>ywaC</i>	2.0796	0.0004	RelA/SpoT domain-containing protein
BCO26_0753	<i>yhaR</i>	2.1031	0.0021	enoyl-CoA hydratase/isomerase
BCO26_2608	<i>kipA</i>	2.1125	0.0087	urea amidolyase-like protein
BCO26_1276	<i>odhB</i>	2.1401	0.0019	2-oxoglutarate dehydrogenase, E2 subunit, dihydrolipoamide succinyltransferase
BCO26_2370	-	2.1486	0.0070	anti-sigma-factor antagonist
BCO26_2499	<i>mtbP</i>	2.1487	0.0436	Modification methylase
BCO26_0089	<i>mcsA</i>	2.1513	0.0467	UvrB/UvrC protein
BCO26_1679	-	2.1551	0.0104	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent
BCO26_2249	-	2.1588	0.0054	hypothetical protein
BCO26_2942	<i>htrC</i>	2.2230	0.0073	peptidase S1 and S6 chymotrypsin/Hap
BCO26_1769	<i>ysfB</i>	2.2363	0.0246	transcriptional regulator CdaR
BCO26_2562	<i>bdhA</i>	2.2874	0.0001	alcohol dehydrogenase zinc-binding domain-containing protein
BCO26_0542	<i>levF</i>	2.2885	0.0036	phosphotransferase system PTS sorbose-specific IIC subunit
BCO26_2541	-	2.2965	0.0467	SMC domain-containing protein
BCO26_2741	<i>sigB</i>	2.3006	0.0001	Sig B/F/G subfamily RNA polymerase sigma-28 subunit
BCO26_0241	<i>gabD</i>	2.3475	0.0002	succinic semialdehyde dehydrogenase
BCO26_0171	<i>argI</i>	2.3475	0.0271	arginase
BCO26_1428	<i>exoAA</i>	2.3652	0.0105	exodeoxyribonuclease III
BCO26_1353	-	2.3995	0.0194	hypothetical protein
BCO26_2824	<i>yhcG</i>	2.4143	0.0351	ABC transporter-like protein
BCO26_1771	-	2.4602	0.0019	heat shock protein Hsp20

BCO26_1419	<i>rtp</i>	2.4726	0.0436	replication terminator protein
BCO26_2570	<i>rbsK</i>	2.4936	0.0237	ribokinase
BCO26_0895	<i>yueB</i>	2.4990	0.0116	hypothetical protein
BCO26_0543	<i>levG</i>	2.5090	0.0049	PTS system, mannose/fructose/sorbose family, IID subunit
BCO26_0541	-	2.5409	0.0001	PTS system, mannose/fructose/sorbose family, IIA subunit
BCO26_0590	-	2.6812	0.0481	hypothetical protein
BCO26_0591	-	2.6841	0.0036	NADPH-dependent FMN reductase
BCO26_1635	<i>yqiW</i>	2.6885	0.0077	hypothetical protein
BCO26_2944	<i>yyclI</i>	2.7032	0.0000	YyclI protein
BCO26_3000		2.7343	0.0194	putative transposase
BCO26_0474	<i>yvfl</i>	2.7422	0.0018	GntR domain-containing protein
BCO26_2742	<i>rsbW</i>	2.7626	0.0000	putative anti-sigma regulatory factor, serine/threonine protein kinase
BCO26_2743	<i>rsbV</i>	2.8194	0.0000	anti-sigma-factor antagonist
BCO26_2424	<i>yteA</i>	2.8282	0.0001	TraR/DksA family transcriptional regulator
BCO26_0740	-	2.8361	0.0000	hypothetical protein
BCO26_2980	-	2.9117	0.0000	hypothetical protein BcoaDRAFT_4102
BCO26_0934	<i>clpE</i>	2.9677	0.0234	ATPase AAA-2 domain-containing protein
BCO26_2825	-	2.9723	0.0001	GntR family transcriptional regulator
BCO26_0737	-	2.9815	0.0005	hypothetical protein
BCO26_0739	-	3.0232	0.0000	hypothetical protein
BCO26_0540	<i>levE</i>	3.1100	0.0001	PTS system, mannose/fructose/sorbose family, IIB subunit
BCO26_2725	<i>groES</i>	3.2119	0.0000	chaperonin Cpn10
BCO26_2375	<i>ybfB</i>	3.2466	0.0000	major facilitator superfamily protein
BCO26_2724	<i>groEL</i>	3.3122	0.0000	chaperonin GroEL
BCO26_0781	<i>yhgE</i>	3.3378	0.0000	YhgE/Pip N-terminal domain-containing protein
BCO26_0400	-	3.3643	0.0000	hypothetical protein
BCO26_2022	<i>acsA</i>	3.3911	0.0033	AMP-dependent synthetase and ligase
BCO26_0738	-	3.3949	0.0001	hypothetical protein
BCO26_0780	<i>yhgD</i>	3.4007	0.0000	TetR family transcriptional regulator

BCO26_0399	-	3.4057	0.0000	hypothetical protein
BCO26_2638	<i>gsiB</i>	3.4856	0.0000	general stress protein
BCO26_1964	<i>citZ</i>	3.4935	0.0000	2-methylcitrate synthase/citrate synthase II
BCO26_0880	<i>ykuS</i>	3.5367	0.0000	hypothetical protein
BCO26_2535	<i>katE</i>	3.5737	0.0132	Catalase
BCO26_1318	-	3.6097	0.0000	hypothetical protein
BCO26_1317	<i>cspL</i>	3.6187	0.0000	cold-shock DNA-binding domain-containing protein
BCO26_2573	-	3.6433	0.0000	hypothetical protein
BCO26_2080	<i>dps</i>	3.6944	0.0012	Ferritin Dps family protein
BCO26_2371	-	3.7143	0.0000	hypothetical protein
BCO26_0972	<i>ykzI</i>	3.8006	0.0000	hypothetical protein
BCO26_1896	-	3.9051	0.0075	hypothetical protein
BCO26_0370	-	3.9154	0.0000	alcohol dehydrogenase GroES domain-containing protein
BCO26_2136	-	3.9586	0.0000	short-chain dehydrogenase/reductase SDR
BCO26_2572	-	4.0593	0.0007	hypothetical protein
BCO26_2079	-	4.0609	0.0004	hypothetical protein
BCO26_2925	-	4.1339	0.0000	hypothetical protein
BCO26_2461	-	4.2752	0.0125	hypothetical protein
BCO26_2926	-	4.3365	0.0000	alanine racemase domain-containing protein
BCO26_2860	<i>yfIT</i>	4.4587	0.0000	hypothetical protein
BCO26_1328	<i>yxAB</i>	4.5939	0.0033	polysaccharide pyruvyl transferase
BCO26_2340	-	4.8911	0.0001	hypothetical protein
BCO26_1065	-	-	0.0488	transposase IS4 family protein

*Log₂FC: the logarithm of fold change, **Q-value: adjustment of P-value.

Supplementary Table 2. Down-regulated genes in *B. coagulans* 2-6 by RNA-seq

Locus	Gene	log ₂ FC*	Q-value**	Product
BCO26_1863	<i>comC</i>	-9.4071	0.0036	Prephilin peptidase
BCO26_0208	<i>gntP</i>	-8.2333	0.0196	gluconate transporter
BCO26_1379	<i>yxlA</i>	-6.6937	0.0202	cytosine/purines uracil thiamine allantoin permease
BCO26_1506	<i>pbuX</i>	-6.0585	0.0012	xanthine permease
BCO26_2004	<i>ycgN</i>	-5.3972	0.0000	delta-1-pyrroline-5-carboxylate dehydrogenase
BCO26_0804	<i>yxaH</i>	-4.8155	0.0144	hypothetical protein
BCO26_2663	<i>purS</i>	-4.7138	0.0000	phosphoribosylformylglycinamide synthase, purS
BCO26_2429	<i>yuaF</i>	-4.4123	0.0015	hypothetical protein
BCO26_0140	-	-4.3427	0.0049	hypothetical protein
BCO26_2003	<i>ycgM</i>	-4.2934	0.0000	Proline dehydrogenase
BCO26_0828	-	-4.2739	0.0000	binding-protein-dependent transport systems inner membrane component
BCO26_2660	<i>purF</i>	-4.1184	0.0013	amidophosphoribosyltransferase
BCO26_2659	<i>purM</i>	-4.1062	0.0006	phosphoribosylformylglycinamide cycloligase
BCO26_1866	-	-3.9611	0.0208	Tfp pilus assembly protein ATPase PilM-like protein
BCO26_0639	<i>lytE</i>	-3.9496	0.0064	NLP/P60 protein
BCO26_2658	<i>purN</i>	-3.8162	0.0010	phosphoribosylglycinamide formyltransferase
BCO26_0070	-	-3.7475	0.0228	hypothetical protein
BCO26_2664	<i>purC</i>	-3.7138	0.0000	phosphoribosylaminoimidazole-succinocarboxamide synthase
BCO26_2661	<i>purL</i>	-3.6640	0.0000	phosphoribosylformylglycinamide synthase II
BCO26_2428	<i>yuaG</i>	-3.5600	0.0026	hypothetical protein
BCO26_1865	-	-3.5231	0.0208	Fimbrial assembly family protein
BCO26_0395	-	-3.5059	0.0077	cell envelope-related transcriptional attenuator
BCO26_0982	<i>ctaB</i>	-3.3928	0.0004	protoheme IX farnesyltransferase
BCO26_1441	<i>yhcI</i>	-3.3455	0.0363	hypothetical protein

BCO26_1869	-	-3.2651	0.0285	twitching motility protein
BCO26_1530	<i>panB</i>	-3.1314	0.0000	3-methyl-2-oxobutanoate hydroxymethyltransferase
BCO26_1198	<i>yufO</i>	-2.9613	0.0000	ABC transporter-like protein
BCO26_0872	<i>natB</i>	-2.9289	0.0031	ABC-2 type transporter
BCO26_2467	<i>fruR</i>	-2.8028	0.0234	DeoR family transcriptional regulator
BCO26_2268	<i>pit</i>	-2.7363	0.0005	phosphate transporter
BCO26_1235	<i>cspD</i>	-2.7183	0.0116	cold-shock DNA-binding domain-containing protein
BCO26_0254	<i>czcD</i>	-2.6722	0.0069	cation diffusion facilitator family transporter
BCO26_1529	<i>panC</i>	-2.6180	0.0005	pantoate/beta-alanine ligase
BCO26_0376	<i>lytD</i>	-2.5334	0.0152	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase
BCO26_0312	<i>yubB</i>	-2.5161	0.0009	undecaprenol kinase
BCO26_2931	-	-2.5026	0.0214	polar amino acid ABC transporter inner membrane subunit
BCO26_2798	<i>atpF</i>	-2.4974	0.0009	ATP synthase F0 subunit B
BCO26_0795	-	-2.4424	0.0010	hypothetical protein
BCO26_1871	-	-2.3884	0.0024	hypothetical protein
BCO26_0871	<i>natA</i>	-2.3256	0.0199	ABC transporter-like protein
BCO26_0126	<i>rplP</i>	-2.3083	0.0250	50S ribosomal protein L16
BCO26_1980	<i>ald</i>	-2.2652	0.0125	alanine dehydrogenase
BCO26_1197	<i>yufN</i>	-2.2543	0.0003	basic membrane lipoprotein
BCO26_2802	<i>glyA</i>	-2.2229	0.0105	glycine hydroxymethyltransferase
BCO26_0134	<i>rplR</i>	-2.1865	0.0018	50S ribosomal protein L18
BCO26_2796	<i>atpA</i>	-2.1209	0.0114	ATP synthase F1 subunit alpha
BCO26_1438	<i>mntH</i>	-2.0894	0.0056	Mn2+/Fe2+ transporter, NRAMP family
BCO26_0981	<i>ctaA</i>	-2.0466	0.0481	cytochrome oxidase assembly
BCO26_0640	-	-2.0442	0.0101	methyl-accepting chemotaxis sensory transducer
BCO26_0142	<i>rpsM</i>	-2.0159	0.0302	30S ribosomal protein S13
BCO26_0125	<i>rpsC</i>	-2.0037	0.0245	30S ribosomal protein S3
BCO26_0443	-	-1.9891	0.0116	glycerol dehydrogenase

BCO26_0827	-	-1.9859	0.0053	family 5 extracellular solute-binding protein
BCO26_1125	<i>hslU</i>	-1.9747	0.0015	heat shock protein HslVU, ATPase subunit HslU
BCO26_0132	<i>rpsH</i>	-1.9086	0.0228	30S ribosomal protein S8
BCO26_0135	<i>rpsE</i>	-1.8813	0.0083	30S ribosomal protein S5
BCO26_0530	-	-1.8492	0.0488	hypothetical protein
BCO26_2267	<i>ykaA</i>	-1.8447	0.0281	hypothetical protein
BCO26_1126	<i>codY</i>	-1.8339	0.0467	GTP-sensing pleiotropic transcriptional repressor CodY
BCO26_0531	<i>ldh</i>	-1.7642	0.0254	L-lactate dehydrogenase
BCO26_1253	-	-1.7337	0.0467	methyl-accepting chemotaxis sensory transducer
BCO26_2665	<i>purB</i>	-1.7075	0.0481	adenylosuccinate lyase
BCO26_0660	<i>hag</i>	-1.6965	0.0374	flagellin
BCO26_0670	-	-1.6779	0.0458	Gamma-glutamyltransferase

*Log₂FC: the logarithm of fold change, **Q-value: adjustment of *P*-value.

Supplementary Table 3. Up-regulated proteins in *B. coagulans* 2-6 by iTRAQ

Locus	Gene	log ₂ FC*	Q-value**	Description
BCO26_0136	<i>rpmD</i>	7.0227	0.0220	50S ribosomal protein L30
BCO26_2925	-	5.9648	0.0001	Uncharacterized protein
BCO26_0880	-	5.8541	0.0001	UPF0180 protein BCO26_0880
BCO26_1317	<i>cspL</i>	5.6614	0.0000	Cold-shock DNA-binding domain protein
BCO26_0255	<i>glmS</i>	5.5967	0.3156	Glutamine--fructose-6-phosphate aminotransferase
BCO26_2102	<i>copZ</i>	5.5448	0.0001	Copper ion binding protein
BCO26_2080	-	5.5186	0.0000	Ferritin Dps family protein
BCO26_0548	<i>ysnF</i>	5.4055	0.0000	Uncharacterized protein
BCO26_0504	-	5.2885	0.0000	Uncharacterized protein
BCO26_1740	<i>yfL</i>	5.0693	0.0000	Acylphosphatase (EC 3.6.1.7)
BCO26_0043	-	4.8450	0.0001	Transcriptional regulator, AbrB family
BCO26_0141	<i>infA</i>	4.7946	0.0000	Translation initiation factor IF-1
BCO26_0425	-	4.7523	0.0000	Glycine betaine/L-proline ABC transporter, ATPase subunit
BCO26_1491	<i>yneJ</i>	4.5668	0.0140	Uncharacterized protein
BCO26_2638	<i>gsiB</i>	4.4977	0.0184	General stress protein
BCO26_0441	-	4.4727	0.0025	Uncharacterized protein
BCO26_0164	-	4.4092	0.0000	Cytochrome bd ubiquinol oxidase subunit I
BCO26_2375	-	4.2469	0.0000	Major facilitator superfamily MFS_1
BCO26_0525	-	4.2197	0.0589	Transcriptional regulator
BCO26_1438	<i>mntH</i>	4.1401	0.0000	Divalent metal cation transporter MntH
BCO26_1778	-	4.0029	0.0000	Heat shock protein Hsp20
BCO26_1458	<i>proB</i>	3.9946	0.0007	Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK)
BCO26_0167	-	3.7879	0.0002	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease/ATP-binding protein CydC
BCO26_0423	-	3.7786	0.0005	Substrate-binding region of ABC-type glycine betaine transport system
BCO26_0505	-	3.7451	0.0002	Quinone oxidoreductase, YhdH/YhfP family
BCO26_0921	<i>mrgA</i>	3.5279	0.0005	Ferritin Dps family protein
BCO26_1788	-	3.5157	0.0000	Alkyl hydroperoxide reductase, F subunit
BCO26_2932	<i>mqo</i>	3.5035	0.0000	Probable malate:quinone oxidoreductase
BCO26_0241	-	3.5013	0.0000	Aldehyde dehydrogenase
BCO26_0939	<i>ptsH</i>	3.4935	0.0000	Phosphotransferase system, phosphocarrier protein HPr
BCO26_1725	<i>rpoD</i>	3.4662	0.0004	RNA polymerase sigma factor SigA
BCO26_2724	<i>groEL</i>	3.3843	0.0000	60 kDa chaperonin (GroEL protein) (Protein Cpn60)
BCO26_0166	<i>cydC</i>	3.2730	0.0000	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease/ATP-binding protein CydD
BCO26_0424	-	3.2591	0.0002	Binding-protein-dependent transport systems inner membrane component

BCO26_0610	-	3.2583	0.0005	Uncharacterized protein
BCO26_0300	-	3.1971	0.0001	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
BCO26_0207	<i>treR</i>	3.1921	0.0007	Transcriptional regulator, GntR family
BCO26_0092	<i>radA</i>	3.1826	0.0045	DNA repair protein RadA
BCO26_2962	-	3.0935	0.0029	Uncharacterized protein
BCO26_1721	-	3.0791	0.0011	Uncharacterized protein
BCO26_1748	<i>hrcA</i>	3.0552	0.0007	Heat-inducible transcription repressor HrcA
BCO26_1648	-	3.0521	0.0000	DNA repair protein RecN (Recombination protein N)
BCO26_0240	-	3.0461	0.0001	Anti-sigma-factor antagonist
BCO26_2617	<i>htpG</i>	3.0134	0.0001	Chaperone protein HtpG (Heat shock protein HtpG) (High temperature protein G)
BCO26_2151	-	2.9273	0.0000	NADH:flavin oxidoreductase/NADH oxidase
BCO26_0934	-	2.9246	0.0000	ATPase AAA-2 domain protein
BCO26_1052	-	2.9075	0.0038	Uncharacterized protein
BCO26_2898	-	2.9038	0.0000	Drug resistance transporter, EmrB/QacA subfamily
BCO26_2515	<i>argD</i>	2.9004	0.0742	Multifunctional fusion protein
BCO26_2685	-	2.8904	0.0001	Anion transporter
BCO26_2513	-	2.8499	0.0000	FAD-dependent pyridine nucleotide-disulfide oxidoreductase
BCO26_0308	-	2.8427	0.0003	Metal dependent phosphohydrolase
BCO26_0586	-	2.8244	0.0002	BAAT/Acyl-CoA thioester hydrolase
BCO26_2416	<i>yfkM</i>	2.8229	0.0000	Intracellular protease, PfpI family
BCO26_0589	-	2.8102	0.0000	Aldo/keto reductase
BCO26_0735	-	2.7917	0.0001	Phosphotransferase system, phosphocarrier protein HPr
BCO26_1709	-	2.7618	0.0001	Nucleotidase (EC 3.1.3.-)
BCO26_0496	<i>metC</i>	2.7363	0.0000	Cystathione gamma-synthase
BCO26_0298	<i>glpK</i>	2.6713	0.0032	Glycerol kinase
BCO26_1429	-	2.6689	0.0000	3-hydroxyisobutyrate dehydrogenase
BCO26_1771	-	2.6197	0.0095	Heat shock protein Hsp20
BCO26_1118	<i>sucD</i>	2.5942	0.0000	Succinate--CoA ligase [ADP-forming] subunit alpha (EC 6.2.1.5) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha)
BCO26_2126	-	2.5806	0.0032	PTS system, glucose subfamily, IIA subunit YvyF
BCO26_0653	-	2.5640	0.0020	Aldo/keto reductase
BCO26_2482	<i>yhdN</i>	2.5571	0.0000	NUDIX hydrolase
BCO26_0731	-	2.5548	0.0000	Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)
BCO26_1746	<i>dnaK</i>	2.5337	0.0000	10 kDa chaperonin (GroES protein) (Protein Cpn10)
BCO26_2725	<i>groES</i>	2.5200	0.0153	Peptidase M17 leucyl aminopeptidase domain protein
BCO26_2167	-	2.4931	0.0873	PTS system, mannose/fructose/sorbose family, IIA subunit
BCO26_0541	<i>ptnA</i>	2.4777	0.0000	

BCO26_2743	<i>rsbV</i>	2.4404	0.0001	Anti-sigma factor antagonist
BCO26_1223	<i>mutL</i>	2.4133	0.0002	DNA mismatch repair protein MutL
BCO26_0186	<i>cobB</i>	2.4064	0.0012	NAD-dependent protein deacetylase (EC 3.5.1.-) (Regulatory protein SIR2 homolog)
BCO26_0660	-	2.4053	0.0000	Flagellin
BCO26_0420	<i>galR</i>	2.3949	0.0029	Transcriptional regulator, LacI family
BCO26_0213	-	2.3943	0.0030	Flavodoxin/nitric oxide synthase
BCO26_2103	-	2.3803	0.0026	Uncharacterized protein
BCO26_1978	-	2.3657	0.0001	UPF0173 metal-dependent hydrolase BCO26_1978
BCO26_0259	-	2.3632	0.0000	NAD-dependent epimerase/dehydratase
BCO26_0874	-	2.3489	0.0000	Uncharacterized protein
BCO26_0832	<i>spxA</i>	2.3374	0.0170	Regulatory protein Spx
BCO26_0587	-	2.3109	0.0041	Esterase/lipase-like protein
BCO26_1784	-	2.2983	0.0001	Uncharacterized protein
BCO26_2957	<i>ribH</i>	2.2752	0.0011	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (LS) (Lumazine synthase) (EC 2.5.1.78)
BCO26_0402	<i>yfmJ</i>	2.2720	0.0000	Alcohol dehydrogenase zinc-binding domain protein
BCO26_1841	<i>yrbC</i>	2.2719	0.0000	Probable transcriptional regulatory protein BCO26_1841
BCO26_1768	-	2.2708	0.0020	Glycolate oxidase, subunit GlcD
BCO26_2495	-	2.2634	0.0000	Nitroreductase
BCO26_1789	-	2.2622	0.0000	Peroxiredoxin
BCO26_0938	-	2.2612	0.0032	Uncharacterized protein
BCO26_2307	-	2.2471	0.0001	Ferric uptake regulator, Fur family
BCO26_1359	<i>plsY</i>	2.2396	0.0001	Glycerol-3-phosphate acyltransferase (Acyl-PO4 G3P acyltransferase) (Acyl-phosphate--glycerol-3-phosphate acyltransferase) (G3P acyltransferase) (GPAT) (EC 2.3.1.n3) (Lysophosphatidic acid synthase) (LPA synthase)
BCO26_0780	<i>yhgD</i>	2.2154	0.0005	Transcriptional regulator, TetR family
BCO26_1977	-	2.2027	0.0057	Putative signal transduction protein with CBS and DRTGG domains
BCO26_0622	<i>galK</i>	2.2010	0.0016	Galactokinase (EC 2.7.1.6) (Galactose kinase)
BCO26_2021	-	2.1981	0.0057	Molybdenum ABC transporter, periplasmic molybdate-binding protein
BCO26_1454	<i>selD</i>	2.1598	0.0000	Selenide, water dikinase (EC 2.7.9.3) (Selenium donor protein) (Selenophosphate synthase)
BCO26_1764	<i>aroE</i>	2.1254	0.0024	Shikimate dehydrogenase (NADP(+)) (SDH) (EC 1.1.1.25)
BCO26_0165	<i>cydB</i>	2.1109	0.0004	Cytochrome d ubiquinol oxidase, subunit II
BCO26_1679	-	2.0960	0.0000	Vitamin B12-dependent ribonucleotide reductase (EC 1.17.4.1)
BCO26_0263	-	2.0749	0.0000	Aminotransferase class I and II
BCO26_0171	-	2.0426	0.0001	Arginase (EC 3.5.3.1)

BCO26_2374	-	2.0188	0.0003	Methionine synthase vitamin-B12 independent
BCO26_2212	-	2.0129	0.0000	Catalase (EC 1.11.1.6)
BCO26_1539	-	2.0036	0.0000	Peptidase membrane zinc metallopeptidase putative
BCO26_1117	<i>sucC</i>	1.9921	0.0005	Succinate--CoA ligase [ADP-forming] subunit beta (EC 6.2.1.5) (Succinyl-CoA synthetase subunit beta) (SCS-beta)
BCO26_0544	-	1.9870	0.0002	Uncharacterized protein
BCO26_2279	-	1.9664	0.0042	Extracellular solute-binding protein family 3
BCO26_2070	<i>ytmA</i>	1.9553	0.0001	BAAT/Acyl-CoA thioester hydrolase
BCO26_1964	-	1.9500	0.0016	Citrate synthase
BCO26_0190	-	1.9480	0.0003	Methyl-accepting chemotaxis sensory transducer with Cache sensor
BCO26_2636	-	1.9436	0.0000	Diacylglycerol kinase catalytic region
BCO26_2370	-	1.9399	0.0006	Anti-sigma-factor antagonist
BCO26_0767	<i>yhaH</i>	1.9251	0.0000	Uncharacterized protein
BCO26_2181	<i>lipA</i>	1.9101	0.0002	Lipoyl synthase (EC 2.8.1.8)
BCO26_0434	-	1.8896	0.0002	RmlC-like cupin
BCO26_2878	-	1.8706	0.0000	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.)
BCO26_0543	<i>manN</i>	1.8642	0.0000	PTS system, mannose/fructose/sorbose family, IID subunit
BCO26_2303	-	1.8491	0.0000	Acetolactate synthase, catabolic
BCO26_0306	<i>yqiG</i>	1.8249	0.0000	NADH:flavin oxidoreductase/NADH oxidase
BCO26_2556	-	1.8216	0.0001	Heavy metal translocating P-type ATPase
BCO26_2595	<i>deoC</i>	1.8132	0.0000	Deoxyribose-phosphate aldolase

*Log₂FC : the logarithm of fold change, **Q-value : adjustment of *P*-value.

Supplementary Table 4. Down-regulated proteins in *B. coagulans* 2-6 by iTRAQ

Locus	Gene	log ₂ FC*	Q-value**	Description
BCO26_2160	-	-7.5824	0.0058	Thioesterase superfamily protein
BCO26_0352	-	-7.5092	0.0001	dTDP-4-dehydrorhamnose reductase
BCO26_0361	-	-6.9636	0.3778	Uncharacterized protein
BCO26_2488	<i>ureG</i>	-6.7583	0.0001	Urease accessory protein UreG
BCO26_0519	-	-6.6545	0.0003	Cell envelope-related transcriptional attenuator
BCO26_2428	-	-6.4803	0.0000	Band 7 protein
BCO26_2275	<i>queG</i>	-6.4136	0.0190	Epoxyqueuosine reductase
BCO26_0819	-	-5.9874	0.0077	Oligopeptide/dipeptide ABC transporter, ATPase subunit
BCO26_1048	<i>pyrD</i>	-5.9114	0.0000	Dihydroorotate dehydrogenase
BCO26_0034	<i>spoV</i> <i>G</i>	-5.7888	0.0000	Putative septation protein SpoVG (Stage V sporulation protein G)
BCO26_2663	<i>purS</i>	-5.6376	0.0001	Phosphoribosylformylglycinamide synthase subunit PurS (FGAM synthase)
BCO26_2368	<i>ilvD</i>	-5.5863	0.0004	Dihydroxy-acid dehydratase (DAD) (EC 4.2.1.9)
BCO26_1650	-	-5.5171	0.0000	Hemolysin A
BCO26_2174	-	-5.4611	0.0003	Uncharacterized protein
BCO26_2285	<i>pflA</i>	-5.3524	0.0001	Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)
BCO26_1607	<i>spoII</i> <i>AB</i>	-5.0539	0.0028	Anti-sigma F factor (EC 2.7.11.1) (Stage II sporulation protein AB)
BCO26_1393	<i>yfiR</i>	-4.9993	0.0045	Transcriptional regulator, TetR family
BCO26_0894	<i>yfjA</i>	-4.8611	0.0008	ESAT-6-like protein
BCO26_1282	-	-4.8083	0.0000	UPF0176 protein BCO26_1282
BCO26_0828	-	-4.7767	0.0000	Binding-protein-dependent transport systems inner membrane component
BCO26_1240	-	-4.7517	0.0001	ABC transporter related protein
BCO26_1484	<i>cspD</i>	-4.7356	0.0002	Cold-shock DNA-binding domain protein
BCO26_1941	-	-4.6901	0.0043	2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)
BCO26_1608	-	-4.6612	0.0000	Anti-sigma F factor antagonist (Stage II sporulation protein)
BCO26_1403	-	-4.6556	0.0012	Transcriptional regulator, MerR family
BCO26_2618	-	-4.6063	0.0002	Terpenoid cyclases/Protein prenyltransferase
BCO26_1933	-	-4.5611	0.0000	tRNA/rRNA methyltransferase (SpoU)
BCO26_2665	-	-4.5541	0.0001	Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)
BCO26_1864	-	-4.5241	0.0064	Uncharacterized protein
BCO26_0555	-	-4.4862	0.0001	ABC transporter related protein
BCO26_0347	-	-4.3992	0.0004	Putative glycosyl transferase
BCO26_0280	-	-4.3586	0.0001	TPR-like protein
BCO26_2119	-	-4.3128	0.0000	Polysaccharide deacetylase
BCO26_2310	-	-4.2956	0.0278	ATP/cobalamin adenosyltransferase
BCO26_1507	<i>xpt</i>	-4.2842	0.0002	Xanthine phosphoribosyltransferase (XPRTase)

				(EC 2.4.2.22)
BCO26_0443	<i>ypjH</i>	-4.2763	0.0000	Glycerol dehydrogenase
BCO26_2156	-	-4.2631	0.0000	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)
BCO26_1894	<i>ysoA</i>	-4.1856	0.0001	TPR-like protein
BCO26_0075	-	-4.1131	0.0001	Deoxynucleoside kinase
BCO26_0584	-	-4.1129	0.0000	Cof-like hydrolase
BCO26_1556	<i>ndk</i>	-4.0916	0.0915	Nucleoside diphosphate kinase (NDK) (NDP kinase) (EC 2.7.4.6) (Nucleoside-2-P kinase)
BCO26_1044	<i>pyrC</i>	-4.0482	0.0004	Dihydroorotase (DHOase) (EC 3.5.2.3)
BCO26_1036	-	-4.0019	0.0027	RNA-binding S4 domain protein
BCO26_1043	<i>pyrB</i>	-3.9945	0.0000	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase)
BCO26_1856	<i>minC</i>	-3.9420	0.0001	Probable septum site-determining protein MinC
BCO26_2364	<i>leuA</i>	-3.8793	0.0752	2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-IPM synthase) (Alpha-isopropylmalate synthase)
BCO26_0567	-	-3.8746	0.0001	Aldehyde-alcohol dehydrogenase
BCO26_1371	-	-3.8619	0.0029	2-nitropropane dioxygenase NPD
BCO26_0726	-	-3.8503	0.0000	HAD-superfamily hydrolase, subfamily IA, variant 1
BCO26_2917	-	-3.8472	0.0001	TIGR00697: conserved hypothetical integral
BCO26_0670	-	-3.7142	0.0003	Gamma-glutamyltransferase
BCO26_0343	-	-3.7141	0.0002	NAD-dependent epimerase/dehydratase
BCO26_1529	<i>panC</i>	-3.6906	0.0001	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)
BCO26_2768	<i>mall</i>	-3.6481	0.0000	Oligo-1,6-glucosidase
BCO26_1408	<i>acoC</i>	-3.6025	0.0162	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.-)
BCO26_1049	<i>pyrF</i>	-3.5786	0.0008	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase) (OMPDCase) (OMPdecase)
BCO26_1045	<i>carA</i>	-3.5253	0.0000	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)
BCO26_1173	<i>rimP</i>	-3.4935	0.0012	Ribosome maturation factor RimP
BCO26_0829	<i>oppC</i>	-3.4615	0.0000	Binding-protein-dependent transport systems inner membrane component
BCO26_1722	-	-3.4578	0.0028	Uncharacterized protein
BCO26_1652	-	-3.4278	0.0087	Polyprenyl synthetase
BCO26_2619	-	-3.4053	0.0003	Uncharacterized protein
BCO26_2545	-	-3.3487	0.0322	Type I site-specific deoxyribonuclease, HsdR family
BCO26_0296	-	-3.3480	0.0006	Glycerol uptake operon antiterminator regulatory protein
BCO26_0202	-	-3.3374	0.0006	Glycine betaine/L-proline ABC transporter, ATPase subunit

BCO26_1166	<i>uppS</i>	-3.3127	0.0014	Isoprenyl transferase (EC 2.5.1.-)
BCO26_1632	-	-3.2619	0.0023	CheW protein
BCO26_0871	-	-3.2586	0.0004	ABC transporter related protein
BCO26_1040	<i>lspA</i>	-3.2580	0.0002	Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal peptidase) (Signal peptidase II) (SPase II)
BCO26_1384	<i>thiE</i>	-3.2397	0.0000	Thiamine-phosphate synthase (TP synthase) (TPS) (EC 2.5.1.3) (Thiamine-phosphate pyrophosphorylase) (TMP pyrophosphorylase) (TMP-PPase)
BCO26_1942	-	-3.1936	0.0043	NADPH-dependent FMN reductase
BCO26_1831	<i>yrzD</i>	-3.1820	0.0392	Uncharacterized protein
BCO26_1720	<i>ispH</i>	-3.1819	0.0004	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.7.4)
BCO26_0831	-	-3.1643	0.0001	ABC transporter related protein
BCO26_0678	-	-3.1311	0.0000	Peptidase M23
BCO26_0568	<i>deaD</i>	-3.1212	0.0000	DEAD/DEAH box helicase domain protein
BCO26_1386	<i>yfIK</i>	-3.1057	0.0050	MOSC domain containing protein
BCO26_2362	<i>leuC</i>	-3.1016	0.0001	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Alpha-IPM isomerase) (IPMI) (Isopropylmalate isomerase)
BCO26_2873	-	-3.0291	0.0000	Uncharacterized protein
BCO26_0174	<i>ybbM</i>	-3.0113	0.0027	Putative transmembrane anti-sigma factor
BCO26_1761	-	-2.9811	0.0247	Metal dependent phosphohydrolase
BCO26_0532	-	-2.9766	0.0004	3D domain protein
BCO26_1544	<i>qcrA</i>	-2.8935	0.0102	Rieske (2Fe-2S) domain protein
BCO26_2123	-	-2.8916	0.0000	Rhodanese domain protein
BCO26_2657	<i>purH</i>	-2.8563	0.0008	Bifunctional purine biosynthesis protein PurH [Includes: IMP cyclohydrolase (EC 3.5.4.10) (IMP synthase) (Inosinicase) (ATIC); Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformylase)]
BCO26_1657	<i>nusB</i>	-2.8266	0.0001	N utilization substance protein B homolog (Protein NusB)
BCO26_2903	<i>deoC</i>	-2.8003	0.0000	Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase) (Deoxyriboaldolase)
BCO26_1314	<i>msrA</i>	-2.7925	0.0000	Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase) (Peptide Met(O) reductase)
BCO26_0638	-	-2.7451	0.0000	Uncharacterized protein
BCO26_1200	-	-2.7242	0.0001	Inner-membrane translocator
BCO26_0203	-	-2.7112	0.0000	Substrate-binding region of ABC-type glycine betaine transport system
BCO26_1992	-	-2.6967	0.0000	AMP-dependent synthetase and ligase
BCO26_2924	-	-2.6938	0.0002	Carboxynorspermidine decarboxylase

BCO26_0811	-	-2.6897	0.0007	Uncharacterized protein
BCO26_0872	<i>yhaP</i>	-2.6678	0.0003	ABC-2 type transporter
BCO26_2688	-	-2.6461	0.0000	Uncharacterized protein
BCO26_0830	-	-2.6101	0.0000	Oligopeptide/dipeptide ABC transporter, ATPase subunit
BCO26_1497	<i>ynzC</i>	-2.6075	0.0001	UPF0291 protein BCO26_1497
BCO26_0728	-	-2.5846	0.0022	Tetratricopeptide TPR_2 repeat protein
BCO26_2922	-	-2.5739	0.0001	Anti-sigma-factor antagonist
BCO26_2664	<i>purC</i>	-2.5465	0.0000	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)
BCO26_2491	<i>ureC</i>	-2.5391	0.0001	Urease subunit alpha (EC 3.5.1.5) (Urea amidohydrolase subunit alpha)
BCO26_0304	-	-2.5149	0.0000	Uncharacterized protein
BCO26_2547	-	-2.4971	0.0004	Type I restriction-modification system, M subunit
BCO26_1936	-	-2.4754	0.0001	Uncharacterized protein
BCO26_2592	<i>guaC</i>	-2.4506	0.0000	GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase) (Guanosine monophosphate reductase)
BCO26_1797	<i>udk</i>	-2.4486	0.0129	Uridine kinase (EC 2.7.1.48) (Cytidine monophosphokinase) (Uridine monophosphokinase)
BCO26_1601	-	-2.4359	0.0000	Diaminopimelate decarboxylase (EC 4.1.1.20)
BCO26_2821	-	-2.4351	0.0008	Response regulator receiver protein
BCO26_0554	-	-2.4201	0.0002	NMT1/THI5 like domain protein
BCO26_2649	<i>pcrA</i>	-2.4122	0.0003	DNA helicase (EC 3.6.4.12)
BCO26_1775	-	-2.4005	0.0007	SirA family protein
BCO26_0345	-	-2.3925	0.0003	Putative lipopolysaccharide biosynthesis protein
BCO26_1046	<i>carB</i>	-2.3867	0.0001	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
BCO26_2739	-	-2.3688	0.0000	RNA binding S1 domain protein
BCO26_2384	-	-2.3454	0.0000	Chromosome segregation ATPase-like protein
BCO26_2950	<i>dnaC</i>	-2.3363	0.0042	Replicative DNA helicase (EC 3.6.4.12)
BCO26_2606	-	-2.3146	0.0003	Uncharacterized protein
BCO26_1890	<i>lonA</i>	-2.3133	0.0000	Lon protease (EC 3.4.21.53) (ATP-dependent protease La)
BCO26_0057	<i>hprt</i>	-2.2931	0.0000	Hypoxanthine phosphoribosyltransferase
BCO26_1527	-	-2.2737	0.0126	DnaQ family exonuclease/DinG family helicase
BCO26_1243	-	-2.2705	0.0000	Uncharacterized protein
BCO26_0391	-	-2.2550	0.0013	Arabinogalactan endo-beta-1,4-galactanase (EC 3.2.1.89)
BCO26_2814	<i>tdk</i>	-2.2521	0.0000	Thymidine kinase (EC 2.7.1.21)
BCO26_0232	-	-2.2426	0.0001	Periplasmic binding protein
BCO26_0348	-	-2.2171	0.0002	NAD-dependent epimerase/dehydratase
BCO26_1953	<i>dnaB</i>	-2.2143	0.0031	Replication initiation and membrane

				attachment family protein
BCO26_2386	-	-2.2108	0.0136	Uncharacterized protein
BCO26_1435	-	-2.2091	0.0004	DSBA oxidoreductase
BCO26_1927	-	-2.1915	0.0004	Cell division protein ZapA
BCO26_1230	<i>hflX</i>	-2.1667	0.0000	GTPase HflX (GTP-binding protein HflX)
BCO26_2476	<i>rlmN</i>	-2.1596	0.0000	Probable dual-specificity RNA methyltransferase RlmN (EC 2.1.1.192) (23S rRNA (adenine(2503)-C(2))-methyltransferase) (23S rRNA m2A2503 methyltransferase) (Ribosomal RNA large subunit methyltransferase N) (tRNA (adenine(37)-C(2))-methyltransferase) (tRNA m2A37 methyltransferase)
BCO26_2304	-	-2.1399	0.0008	Transcriptional regulator, LysR family
BCO26_2608	-	-2.1276	0.0236	Urea amidolyase related protein
BCO26_2644	-	-2.1254	0.0003	Malate synthase (EC 2.3.3.9)
BCO26_1050	<i>pyrE</i>	-2.1166	0.0000	Orotate phosphoribosyltransferase (OPRT) (OPRTase) (EC 2.4.2.10)
BCO26_2693	-	-2.1107	0.0000	Transposase IS4 family protein
BCO26_0427	-	-2.0539	0.0000	Transferase hexapeptide repeat containing protein
BCO26_0083	-	-2.0469	0.0021	Uncharacterized protein
BCO26_1810	<i>mnmA</i>	-2.0469	0.0017	tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.13)
BCO26_2648	<i>pcrA</i>	-2.0207	0.0001	DNA helicase (EC 3.6.4.12)
BCO26_1922	-	-2.0203	0.0003	Transcriptional regulator, TetR family
BCO26_1101	<i>smc</i>	-2.0146	0.0000	Chromosome partition protein Smc
BCO26_1687	<i>aroK</i>	-2.0087	0.0011	Shikimate kinase (SK) (EC 2.7.1.71)
BCO26_1998	-	-1.9980	0.0005	Putative GAF sensor protein
BCO26_1636	<i>fruK</i>	-1.9887	0.0003	1-phosphofructokinase
BCO26_0019	-	-1.9715	0.0035	Methyltransferase small
BCO26_1509	-	-1.9706	0.0001	Putative RNA methylase
BCO26_2801	<i>upp</i>	-1.9023	0.0000	Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)
BCO26_0267	-	-1.8989	0.0008	UPF0210 protein BCO26_0267
BCO26_1112	-	-1.8932	0.0001	Signal peptidase I (EC 3.4.21.89)
BCO26_2472	<i>yxeH</i>	-1.8477	0.0000	Cof-like hydrolase
BCO26_1008	<i>bshC</i>	-1.7849	0.0000	Putative cysteine ligase BshC (EC 6.---)

*Log₂FC: the logarithm of fold change, **Q-value: adjustment of P-value.

Supplementary Table 5. Commonly differentially accumulated in the RNA-seq and iTRAQ

Locus	Gene	$\log_2(37/60)$	Product
BCO26_2925	-	5.96	hypothetical protein
BCO26_0880	<i>ykuS</i>	5.85	hypothetical protein
BCO26_1317	<i>cspL</i>	5.66	cold-shock DNA-binding domain-containing protein
BCO26_2080	<i>dps</i>	5.51	Ferritin dps family protein
BCO26_2638	<i>gsiB</i>	4.49	general stress protein
BCO26_2375	<i>ybfB</i>	4.24	major facilitator superfamily protein
BCO26_1438	<i>mntH</i>	4.14	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
BCO26_2932	-	3.50	malate/quinone oxidoreductase
BCO26_0241	<i>gabD</i>	3.50	
BCO26_2724	<i>groEL</i>	3.38	chaperonin GroEL
BCO26_1748	<i>hrcA</i>	3.05	heat-inducible transcription repressor HrcA
BCO26_0934	<i>clpE</i>	2.92	ATPase AAA-2 domain-containing protein
BCO26_1771	-	2.61	heat shock protein Hsp20
BCO26_1746	<i>dnaK</i>	2.53	chaperone protein DnaK
BCO26_2725	<i>groES</i>	2.51	chaperonin Cpn10
BCO26_0541	-	2.47	PTS system, mannose/fructose/sorbose family, IIA subunit
BCO26_2743	<i>rsbV</i>	2.44	anti-sigma-factor antagonist
BCO26_0660	<i>hag</i>	2.40	flagellin
BCO26_0780	<i>yhgD</i>	2.21	TetR family transcriptional regulator
BCO26_1679	-	2.09	adenosylcobalamin-dependent ribonucleoside-diphosphate reductase
BCO26_0171	<i>argI</i>	2.04	arginase
BCO26_1117	<i>sucC</i>	1.99	succinyl-CoA synthetase subunit beta
BCO26_1964	<i>citZ</i>	1.94	2-methylcitrate synthase/citrate synthase II
BCO26_2370	-	1.93	anti-sigma-factor antagonist
BCO26_0543	<i>levG</i>	1.86	PTS system, mannose/fructose/sorbose family, IID subunit
BCO26_0306	<i>yqiG</i>	1.82	NADH:flavin oxidoreductase/NADH oxidase
BCO26_2608	<i>kipA</i>	-2.12	urea amidolyase-like protein
BCO26_2664	<i>purC</i>	-2.54	phosphoribosylaminoimidazole-succinocarboxamide synthase
BCO26_0872	<i>natB</i>	-2.66	ABC-2 type transporter
BCO26_0639	<i>lytE</i>	-2.74	NLP/P60 protein
BCO26_0871	<i>natA</i>	-3.25	ABC transporter-like protein
BCO26_1529	<i>panC</i>	-3.69	pantoate/beta-alanine ligase
BCO26_0670	-	-3.71	gamma-glutamyltransferase
BCO26_0443	-	-4.27	glycerol dehydrogenase
BCO26_2665	<i>purB</i>	-4.55	adenylosuccinate lyase
BCO26_0828	-	-4.77	binding-protein-dependent transport systems inner membrane component
BCO26_2663	<i>purS</i>	-5.63	phosphoribosylformylglycinamidine synthase, purS
BCO26_2428	<i>yuaG</i>	-6.48	hypothetical protein

Supplementary Table 6. mRNA targets of CspL in *E. coli* DH5 α by RIP-seq

Gene	Description	Foldchange	P-Value
<i>acpP</i>	acyl carrier protein (ACP)	3.209574	0.011899
<i>acrE</i>	cytoplasmic membrane lipoprotein	5.40998	0.033148
<i>acrF</i>	multidrug efflux system protein	3.447072	0.02446
<i>actP</i>	acetate transporter	5.017942	0.000673
<i>ahpC</i>	alkyl hydroperoxide reductase, C22 subunit	6.277318	0.00017
<i>aslB</i>	putative AslA-specific sulfatase-maturating enzyme	4.007795	0.010328
<i>aspA</i>	aspartate ammonia-lyase	3.189925	0.01204
<i>atoB</i>	acetyl-CoA acetyltransferase	3.056902	0.021741
<i>atpC</i>	F1 sector of membrane-bound ATP synthase, epsilon subunit	8.418546	1.64E-05
<i>bamB</i>	BamABCDE complex OM biogenesis lipoprotein	5.713884	0.000256
<i>bax</i>	putative glucosaminidase	4.753606	0.000945
<i>bolA</i>	stationary-phase morphogene, transcriptional repressor for mreB; also regulator for dacA, dacC, and ampC	3.849887	0.003751
<i>bssS</i>	biofilm regulator	2.773061	0.025726
<i>chbC</i>	N,N'-diacetylchitobiose-specific enzyme IIC component of PTS	4.538809	0.007841
<i>citX</i>	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	13.08699	0.000935
<i>creC</i>	sensory histidine kinase in two-component regulatory system with CreB or PhoB	3.46148	0.032593
<i>cspC</i>	stress protein, member of the CspA-family	5.556331	0.000546
<i>cspE</i>	constitutive cold shock family transcription antitermination protein; negative regulator of cspA transcription; RNA melting protein; ssDNA-binding protein	7.54401	4.64E-05
<i>cutC</i>	copper homeostasis protein	6.964267	6.17E-05
<i>cynX</i>	putative cyanate transporter	9.186281	0.00679
<i>ddpC</i>	D,D-dipeptide ABC transporter permease	8.085941	0.004943
<i>diaA</i>	DnaA initiator-associating factor for replication initiation	3.495332	0.019935
<i>dtpC</i>	dipeptide and tripeptide permease	3.676945	0.024268
<i>dusB</i>	tRNA-dihydrouridine synthase B	5.506834	0.00128
<i>ecpA</i>	ECP pilin	31.32438	3.33E-05
<i>elyC</i>	envelope biogenesis factor; DUF218 superfamily protein	3.134626	0.039049
<i>eno</i>	enolase	2.523128	0.042581
<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein]	3.019607	0.016262
<i>fabZ</i>	(3R)-hydroxymyristol acyl carrier protein dehydratase	3.161011	0.019625
<i>fdhF</i>	formate dehydrogenase-H, selenopolypeptide subunit	2.570259	0.041695
<i>fdrA</i>	putative NAD(P)-binding acyl-CoA synthetase	10.48652	0.003397
<i>fetB</i>	iron export ABC transporter permease; peroxide resistance protein	4.323343	0.010321
<i>fhuA</i>	ferrichrome outer membrane transporter	3.385106	0.009279
<i>frdD</i>	fumarate reductase (anaerobic), membrane anchor subunit	4.378659	0.003917
<i>frlD</i>	fructoselysine 6-kinase	4.350342	0.016253
<i>frwD</i>	putative enzyme IIB component of PTS	6.585809	0.029994
<i>ftsB</i>	cell division protein	2.929617	0.039821
<i>fucI</i>	L-fucose isomerase	3.423418	0.013042

<i>gadX</i>	acid resistance regulon transcriptional activator; autoactivator	3.434245	0.009939
<i>gfcC</i>	putative O-antigen capsule production periplasmic protein	6.585809	0.029994
<i>glgS</i>	motility and biofilm regulator	4.199755	0.002111
<i>glnB</i>	regulatory protein P-II for glutamine synthetase	4.187669	0.02311
<i>glvBC</i>	arbutin specific enzyme IIIBC component of PTS	4.966913	0.020774
<i>grcA</i>	autonomous glycyl radical cofactor	3.77471	0.008271
<i>greB</i>	transcript cleavage factor	7.706497	0.001895
<i>gspH</i>	putative general secretory pathway component, cryptic	62.45439	0.002355
<i>hns</i>	global DNA-binding transcriptional dual regulator H-NS	7.787963	2.09E-05
<i>hofB</i>	T2SE secretion family protein; P-loop ATPase superfamily protein	3.192656	0.041713
<i>hokD</i>	Qin prophage; small toxic polypeptide	833.1739	2.46E-21
<i>hpf</i>	ribosome hibernation promoting factor HPF; stabilizes 100S dimers	3.038436	0.021803
<i>hspQ</i>	heat shock protein involved in degradation of mutant DnaA; hemimethylated oriC DNA-binding protein	2.819931	0.024334
<i>hupB</i>	HU, DNA-binding transcriptional regulator, beta subunit	8.143978	2.46E-05
<i>hybD</i>	maturity protease for hydrogenase 2	3.668497	0.01606
<i>hyfG</i>	hydrogenase 4, subunit	8.62491	9.06E-05
<i>ibaG</i>	acid stress protein; putative BolA family transcriptional regulator	6.585809	0.029994
<i>ibsD</i>	toxic membrane protein	5.40998	0.033148
<i>insA-20</i>	IS1 protein InsA	5.40998	0.033148
<i>insF-2</i>	IS3 element protein InsF	17.00581	3.62E-05
<i>iscX</i>	Fe(2+) donor and activity modulator for cysteine desulfurase	3.46148	0.032593
<i>lpp</i>	murein lipoprotein	20.37404	4.48E-09
<i>lpxA</i>	UDP-N-acetylglucosamine acetyltransferase	5.159657	0.001008
<i>lpxB</i>	tetraacyldisaccharide-1-P synthase	3.344291	0.018232
<i>lpxC</i>	UDP-3-O-acyl N-acetylglucosamine deacetylase	6.350676	0.000112
<i>lpxD</i>	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	3.271445	0.013084
<i>lspA</i>	prolipoprotein signal peptidase (signal peptidase II)	4.139157	0.006016
<i>marB</i>	periplasmic mar operon regulator	12.14387	0.009409
<i>mcrC</i>	5-methylcytosine-specific restriction enzyme McrBC, subunit McrC	16.939	0.001795
<i>mepS</i>	murein DD-endopeptidase, space-maker hydrolase, mutational suppressor of prc thermosensitivity, outer membrane lipoprotein, weak murein LD-carboxypeptidase	3.217454	0.042785
<i>metJ</i>	transcriptional repressor, S-adenosylmethionine-binding	3.84058	0.034643
<i>mlaA</i>	ABC transporter maintaining OM lipid asymmetry, OM lipoprotein component	2.742079	0.031826
<i>mltD</i>	putative membrane-bound lytic murein transglycosylase D	6.158456	0.000168
<i>mokB</i>	regulatory peptide	3.337777	0.024422
<i>mokC</i>	regulatory protein for HokC	62.45439	0.002355
<i>mreC</i>	cell wall structural complex MreBCD transmembrane component MreC	3.16955	0.021326
<i>mreD</i>	cell wall structural complex MreBCD transmembrane component MreD	4.623171	0.02182

<i>nadB</i>	quinolinate synthase, L-aspartate oxidase (B protein) subunit	2.9327	0.028079
<i>nagC</i>	N-acetylglucosamine-inducible nag divergent operon transcriptional repressor	2.972479	0.025544
<i>nrdH</i>	hydrogen donor for NrdEF electron transport system; glutaredoxin-like protein	4.796089	0.034567
<i>osmE</i>	osmotically-inducible lipoprotein	8.729785	1.06E-05
<i>pcnB</i>	poly(A) polymerase	2.971236	0.048139
<i>pdhR</i>	pyruvate dehydrogenase complex repressor; autorepressor	2.719794	0.038463
<i>pgaB</i>	poly-beta-1,6-N-acetyl-D-glucosamine (PGA) N-deacetylase outer membrane export lipoprotein	3.84058	0.034643
<i>pgrR</i>	murein peptide degradation regulator	3.318453	0.046767
<i>pitB</i>	phosphate transporter	5.51483	0.012477
<i>pnp</i>	polynucleotide phosphorylase/polyadenylase	4.463405	0.001525
<i>priB</i>	primosomal protein N	7.538298	0.000998
<i>purA</i>	adenylosuccinate synthetase	2.748753	0.034027
<i>rhsB</i>	Rhs protein with DUF4329 family putative toxin domain; putative neighboring cell growth inhibitor	3.246389	0.024304
<i>rmf</i>	ribosome modulation factor	51.17602	8.01E-13
<i>rof</i>	modulator of Rho-dependent transcription termination	2.987261	0.019071
<i>rplA</i>	50S ribosomal subunit protein L1	2.731246	0.030338
<i>rplI</i>	50S ribosomal subunit protein L9	5.732205	0.000532
<i>rplK</i>	50S ribosomal subunit protein L11	2.582293	0.04626
<i>rplQ</i>	50S ribosomal subunit protein L17	4.581168	0.001313
<i>rplT</i>	50S ribosomal subunit protein L20	4.593493	0.001203
<i>rpmA</i>	50S ribosomal subunit protein L27	2.687881	0.035911
<i>rpmB</i>	50S ribosomal subunit protein L28	5.541826	0.00872
<i>rpmG</i>	50S ribosomal subunit protein L33	8.80233	0.000807
<i>rpmI</i>	50S ribosomal subunit protein L35	4.446064	0.003241
<i>rpoA</i>	RNA polymerase, alpha subunit	2.493898	0.045829
<i>rpoE</i>	RNA polymerase sigma E factor	3.447987	0.00876
<i>rpsB</i>	30S ribosomal subunit protein S2	3.134611	0.013402
<i>rpsF</i>	30S ribosomal subunit protein S6	4.51296	0.004869
<i>rpsK</i>	30S ribosomal subunit protein S11	2.499139	0.0493
<i>rpsO</i>	30S ribosomal subunit protein S15	3.409615	0.008777
<i>rpsQ</i>	30S ribosomal subunit protein S17	3.992406	0.004247
<i>rpsR</i>	30S ribosomal subunit protein S18	12.14387	0.009409
<i>rpsT</i>	30S ribosomal subunit protein S20	6.177334	0.000578
<i>rpsU</i>	30S ribosomal subunit protein S21	13.34723	4.18E-07
<i>rraA</i>	ribonuclease E (RNase E) inhibitor protein	3.913945	0.003444
<i>rsmE</i>	16S rRNA m(3)U1498 methyltransferase, SAM-dependent	4.760002	0.008624
<i>rspB</i>	putative Zn-dependent NAD(P)-binding oxidoreductase	3.044887	0.034497
<i>ryfB</i>	hypothetical protein	6.352104	0.002965
<i>rzpD</i>	DLP12 prophage; putative murein endopeptidase	4.418997	0.035098
<i>secE</i>	preprotein translocase membrane subunit	3.01071	0.026356
<i>secG</i>	preprotein translocase membrane subunit	8.602427	6.06E-05
<i>sieB</i>	phage superinfection exclusion protein, Rac prophage	3.941004	0.014502

<i>skp</i>	periplasmic chaperone	3.276121	0.012614
<i>ssb</i>	single-stranded DNA-binding protein	4.722417	0.001074
<i>symE</i>	toxic peptide regulated by antisense sRNA symR	5.51483	0.012477
<i>tdcA</i>	tdc operon transcriptional activator	7.886045	0.014032
<i>torY</i>	TMAO reductase III (TorYZ), cytochrome c-type subunit	3.415476	0.02446
<i>trxA</i>	thioredoxin 1	6.090052	0.000161
<i>uxuB</i>	D-mannose oxidoreductase, NAD-dependent	2.959111	0.029658
<i>vioB</i>	VioB, involved in dTDP-N-acetylviosamine synthesis	3.51241	0.032995
<i>waaV</i>	putative beta1,3-glucosyltransferase	3.267396	0.030569
<i>wcaD</i>	putative colanic acid polymerase	17.00581	3.62E-05
<i>xthA</i>	exonuclease III	5.962049	0.000976
<i>xylE</i>	D-xylose transporter	2.712545	0.036868
<i>yaaW</i>	UPF0174 family protein	4.187669	0.02311
<i>yadV</i>	putative periplasmic pilin chaperone	7.886045	0.014032
<i>ybcJ</i>	ribosome-associated protein; putative RNA-binding protein	15.29454	3.15E-06
<i>ybcK</i>	DLP12 prophage; putative recombinase	6.206146	0.002108
<i>ybgF</i>	periplasmic TolA-binding protein	2.643229	0.0376
<i>ybjS</i>	putative NAD(P)H-dependent oxidoreductase	2.741351	0.030532
<i>yceD</i>	DUF177 family protein	3.246461	0.021017
<i>ycgI</i>	hypothetical protein	9.746308	0.023263
<i>ycgX</i>	DUF1398 family protein	5.16591	0.009699
<i>yciC</i>	UPF0259 family inner membrane protein	2.94429	0.04277
<i>yciY</i>	uncharacterized protein	42.77316	1.42E-09
<i>ydcC</i>	H repeat-associated putative transposase	5.40998	0.033148
<i>ydcH</i>	DUF465 family protein	2.735667	0.029241
<i>ydeQ</i>	putative fimbrial-like adhesin protein	62.45439	0.002355
<i>ydfK</i>	cold shock protein, function unknown, Qin prophage	3.27404	0.011718
<i>ydhZ</i>	uncharacterized protein	3.093031	0.037005
<i>ydjH</i>	putative kinase	9.746308	0.023263
<i>yebO</i>	putative inner membrane protein	2.834947	0.033672
<i>yech</i>	DUF2492 family protein	3.603295	0.019449
<i>yecT</i>	uncharacterized protein	3.979716	0.034967
<i>yegK</i>	ser/thr phosphatase-related protein	4.534759	0.015553
<i>yfbR</i>	5'-nucleotidase	4.163844	0.035158
<i>yfcJ</i>	putative arabinose efflux transporter	10.33865	4.40E-05
<i>yfcZ</i>	UPF0381 family protein	14.93671	1.38E-06
<i>yfeD</i>	DUF1323 family putative DNA-binding protein	2.764708	0.028824
<i>ygbA</i>	uncharacterized protein	3.316346	0.024402
<i>ygdR</i>	DUF903 family verified lipoprotein	22.50025	5.14E-07
<i>ygfK</i>	putative Fe-S subunit oxidoreductase subunit	7.191291	0.000108
<i>yggD</i>	MtlR family putative transcriptional repressor	3.561411	0.016737
<i>yggI</i>	Zn-dependent metalloprotease-related protein	4.375114	0.022569
<i>yggS</i>	UPF0001 family protein, PLP-binding	3.818282	0.018485
<i>yghR</i>	putative ATP-binding protein	93.18158	0.000319
<i>yghS</i>	putative ATP-binding protein	16.939	0.001795

<i>ygiN</i>	quinol monooxygenase	3.899535	0.004836
<i>ygiZ</i>	inner membrane protein	7.538298	0.000998
<i>ygjI</i>	putative transporter	7.193954	0.009097
<i>yhaB</i>	uncharacterized protein	4.418997	0.035098
<i>yhfX</i>	putative pyridoxal 5'-phosphate binding protein	9.746308	0.023263
<i>yhiKL</i>	hypothetical protein	7.379136	0.001624
<i>yiaB</i>	YiaAB family inner membrane protein	9.746308	0.023263
<i>yifE</i>	UPF0438 family protein	5.89942	0.000473
<i>yihD</i>	DUF1040 protein YihD	4.968943	0.007961
<i>yihL</i>	putative DNA-binding transcriptional regulator	11.78675	0.001755
<i>yjbE</i>	extracellular polysaccharide production threonine-rich protein	16.939	0.001795
<i>yjbJ</i>	stress-induced protein, UPF0337 family	3.500016	0.006655
<i>yjbL</i>	uncharacterized protein	12.14387	0.009409
<i>yjhX</i>	UPF0386 family protein	13.08699	0.000935
<i>yjjV</i>	putative DNase	3.246266	0.030295
<i>ykiA</i>	hypothetical protein	4.619387	0.006433
<i>ymdF</i>	KGG family protein	4.678155	0.007337
<i>ymdF</i>	KGG family protein	3.863167	0.003654
<i>ynaE</i>	cold shock protein, Rac prophage	3.27404	0.011718
<i>ynaJ</i>	DUF2534 family putative inner membrane protein	8.532225	1.26E-05
<i>yneL</i>	putative transcriptional regulator	77.81799	0.000833
<i>yniA</i>	fructosamine kinase family protein	3.659973	0.005595
<i>ynjD</i>	putative ABC transporter ATPase	10.44608	0.000248
<i>ynjI</i>	inner membrane protein	13.08699	0.000935
<i>yqfA</i>	hemolysin III family HylIII inner membrane protein	2.615779	0.03955
<i>yqiA</i>	acyl CoA esterase	3.46148	0.032593
<i>yqiB</i>	DUF1249 protein YqiB	3.447072	0.02446
<i>yraH</i>	putative fimbrial-like adhesin protein	4.406606	0.004523
<i>yraJ</i>	putative outer membrane protein	13.59433	3.22E-07
<i>yrbL</i>	Mg(2+)-starvation-stimulated protein	3.052986	0.034929
<i>ytfK</i>	DUF1107 family protein	3.931535	0.00317
<i>ytfP</i>	GGCT-like protein	3.818045	0.004559
<i>yzfA</i>	hypothetical protein	16.98769	0.000167
<i>zapA</i>	FtsZ stabilizer	8.311171	1.39E-05
<i>ECD_03695</i>	Magnesium and cobalt transport protein corA	3.84058	0.034643
<i>ECD_00840</i>	hypothetical protein	3.379743	0.031841
<i>ECD_03786</i>	putative glycoporin	3.085895	0.02023
<i>ECD_02855</i>	hypothetical protein	3.113105	0.013798
<i>ECD_02652</i>	hypothetical protein	5.51483	0.012477
<i>ECD_02621</i>	hypothetical protein	3.595737	0.011338
<i>ECD_00022</i>	hypothetical protein	12.14387	0.009409
<i>ECD_04314</i>	hypothetical protein	4.474227	0.006136
<i>ECD_00815</i>	integrase for prophage	5.730951	0.000523
<i>ECD_03459</i>	hypothetical protein	93.18158	0.000319

RIP-seq at 45 °C			
<i>aaeR</i>	LysR-typ	2.70218	0.002386
<i>abgR</i>	putative	4.02184	0.000685
<i>acnA</i>	aconitat	2.65249	0.001428
<i>acpT</i>	holo-[ac	3.29464	0.001157
<i>acrF</i>	multidru	4.15713	0.00029
<i>acrR</i>	DNA-bind	2.78407	0.003
<i>adiA</i>	arginine	2.40171	0.005009
<i>adiC</i>	arginine	3.06149	0.00159
<i>adk</i>	adenylat	2.64996	0.003808
<i>agaB</i>	galactos	2.59212	0.003396
<i>agal</i>	putative	2.40951	0.007147
<i>ahpC</i>	alkyl hy	3.13729	0.001461
<i>aidB</i>	putative	3.53302	0.002347
<i>aldA</i>	aldehyde	3.4241	0.001582
<i>alkB</i>	DNA oxid	3.90966	0.00056
<i>allC</i>	allantoa	4.81374	0.000278
<i>alle</i>	(S)-urei	3.96882	0.000801
<i>alsA</i>	D-allose	3.36181	0.000939
<i>alsB</i>	D-allose	3.93246	0.001152
<i>alsE</i>	D-allulo	2.02525	0.019469
<i>ampE</i>	protein	2.47811	0.005142
<i>ampG</i>	muropept	2.2025	0.008454
<i>ansB</i>	L-aspara	3.3805	0.001263
<i>araJ</i>	putative	4.73139	0.000139
<i>arnB</i>	UDP-4-am	3.06372	0.000651
<i>arnT</i>	lipid IV	2.67612	0.004389
<i>aroK</i>	shikimat	2.97643	0.001798
<i>aroL</i>	shikimat	5.06518	0.000299
<i>arpA</i>	regulato	2.9345	0.002394
<i>arpB</i>	EcoGene:	3.34382	0.000953
<i>artJ</i>	L-argini	3.38676	0.001889
<i>artP</i>	L-argini	2.75665	0.002606
<i>ascG</i>	DNA-bind	2.69596	0.002518
<i>asnU</i>	EcoGene:	3.34195	0.001145
<i>asnV</i>	EcoGene:	2.39627	0.003705
<i>atoB</i>	acetyl-C	3.14662	0.001326
<i>atoC</i>	DNA-bind	3.63521	0.000815
<i>atoS</i>	sensory	2.78907	0.002241
<i>bacA</i>	undecapr	2.57686	0.003297
<i>barA</i>	sensory	2.88664	0.001586
<i>bcsE</i>	c-di-GMP	2.73256	0.003566
<i>betT</i>	choline:	2.93847	0.001416
<i>bgIB</i>	6-phosph	2.52141	0.007533
<i>bgIF</i>	beta-glu	2.46536	0.005557

<i>bglH</i>	carbohyd	3.66982	0.000822
<i>bglJ</i>	DNA-bind	2.11218	0.014947
<i>birA</i>	DNA-bind	2.4006	0.004102
<i>bisC</i>	biotin s	4.80925	0.000369
<i>blr</i>	beta-lac	2.02835	0.01479
<i>bolA</i>	DNA-bind	2.36194	0.005649
<i>bsmA</i>	DUF1471	3.96098	0.00021
<i>bssR</i>	regulato	9.68467	3.62E-05
<i>bssS</i>	regulato	5.61678	7.05E-05
<i>cadB</i>	lysine:c	5.31585	0.000224
<i>cadC</i>	DNA-bind	4.1597	0.000466
<i>caiB</i>	gamma-bu	2.73003	0.001757
<i>caiD</i>	crotonob	2.88006	0.002891
<i>caiE</i>	putative	2.64433	0.004484
<i>caiT</i>	L-carnit	4.30431	0.000451
<i>carA</i>	carbamoy	2.79536	0.00266
<i>carB</i>	carbamoy	2.47381	0.008491
<i>cbl</i>	DNA-bind	4.07401	0.000808
<i>cbrB</i>	putative	4.38117	0.000736
<i>cdgI</i>	putative	2.073	0.018846
<i>chaA</i>	Na(+)/K(4.38825	0.000578
<i>chaB</i>	putative	4.54168	0.000272
<i>chbC</i>	N,N'-dia	2.79104	0.006452
<i>chbF</i>	monoacet	3.98321	0.000681
<i>cheR</i>	chemotax	4.16165	0.000581
<i>cheY</i>	chemotax	5.25309	0.000204
<i>cirA</i>	ferric d	3.31654	0.001002
<i>clsC</i>	cardioli	3.82785	0.000814
<i>cmtA</i>	#N/A	3.58701	0.000659
<i>coaD</i>	pantethe	3.72575	0.000418
<i>cobS</i>	cobalami	2.84783	0.002597
<i>codB</i>	cytosine	2.72631	0.003585
<i>creA</i>	PF05981	3.19339	0.001958
<i>csgC</i>	inhibito	5.02313	0.000259
<i>csiD</i>	PF08943	3.17675	0.001703
<i>cspH</i>	CspA fam	2.60107	0.004479
<i>csrA</i>	carbon s	1.71929	0.02066
<i>cueO</i>	cuprous	4.44555	0.00069
<i>curA</i>	NADPH-de	5.66106	0.000254
<i>cyuP</i>	putative	2.42953	0.005765
<i>dacC</i>	D-alanyl	2.23972	0.015482
<i>dacD</i>	D-alanyl	2.05841	0.005227
<i>dcuD</i>	putative	2.15704	0.009668
<i>dcuR</i>	DNA-bind	3.35393	0.00119
<i>ddpC</i>	putative	2.916	0.001877

<i>dedA</i>	DedA fam	3.04368	0.00376
<i>dgcE</i>	putative	2.38774	0.008844
<i>dgcP</i>	diguanyl	2.89353	0.002796
<i>dgcT</i>	putative	4.18798	0.000354
<i>dham</i>	dihydrox	2.99837	0.00286
<i>dinD</i>	DNA dama	2.99214	0.002715
<i>djlC</i>	co-chape	2.24607	0.014512
<i>dkgA</i>	methylgl	3.02762	0.002004
<i>dosP</i>	oxygen-s	3.91871	0.002353
<i>dpiB</i>	sensory	2.64826	0.004124
<i>dsbA</i>	thiol:di	4.06533	0.000419
<i>dsdA</i>	D-serine	3.13886	0.001793
<i>dsdX</i>	D-serine	4.51171	0.000419
<i>dtpC</i>	dipeptid	2.9459	0.001551
<i>eamB</i>	cysteine	3.21816	0.001443
<i>ebgA</i>	evolved	2.45551	0.004941
<i>ebgC</i>	DUF386 d	3.48327	0.001275
<i>ecpA</i>	common p	1.79632	0.010079
<i>efeB</i>	heme-con	6.99246	3.67E-05
<i>efeO</i>	ferrous	2.12892	0.008518
<i>elfC</i>	putative	2.97661	0.003598
<i>elfD</i>	putative	3.35294	0.000921
<i>emrE</i>	multidru	3.30588	0.001783
<i>emrY</i>	triparti	2.27685	0.012723
<i>envC</i>	murein h	3.45236	0.000828
<i>eptA</i>	phosphoe	3.34937	0.001154
<i>essD</i>	DLP12 pr	3.58503	0.001005
<i>evgA</i>	DNA-bind	3.15432	0.001859
<i>fadD</i>	fatty ac	3.89773	0.000431
<i>fadH</i>	2,4-dien	1.92998	0.025425
<i>fadJ</i>	3-hydrox	6.0351	0.000134
<i>fadR</i>	DNA-bind	2.64872	0.003089
<i>feaB</i>	phenylac	2.35576	0.012609
<i>sepE</i>	polysacc	3.03501	0.002756
<i>fes</i>	enteroch	4.04475	0.000706
<i>fhlA</i>	DNA-bind	4.50111	0.000531
<i>fimB</i>	regulato	2.83876	0.004994
<i>fimD</i>	type I f	3.8474	0.00061
<i>fimE</i>	regulato	1.8954	0.035159
<i>fimI</i>	putative	5.65467	0.000136
<i>fimZ</i>	putative	4.17746	0.000284
<i>focB</i>	putative	2.31746	0.005396
<i>folM</i>	dihydrom	2.44774	0.009524
<i>frlR</i>	putative	2.69399	0.002818
<i>frmB</i>	S-formyl	2.21635	0.010534

<i>frwC</i>	putative	3.54824	0.001163
<i>ftsW</i>	putative	4.41123	0.000223
<i>fucO</i>	L-1,2-pr	2.93849	0.002153
<i>fumA</i>	fumarase	3.60624	0.001886
<i>fumD</i>	fumarase	3.07769	0.001758
<i>gadC</i>	L-glutam	3.59373	0.000506
<i>gadY</i>		3.13996	0.00195
<i>galF</i>	UTP:gluc	2.908	0.003627
<i>gapC</i>	EcoGene:	2.77467	0.003874
<i>garP</i>	galactar	3.11508	0.002264
<i>gcl</i>	glyoxyla	2.17704	0.013289
<i>gfcB</i>	lipoprot	3.15644	0.001686
<i>gfcD</i>	putative	3.11352	0.001843
<i>glcA</i>	glycolat	3.50144	0.001344
<i>glcB</i>	malate s	2.09708	0.016584
<i>gloA</i>	glyoxala	4.14622	0.00044
<i>gloB</i>	hydroxya	5.43372	3.88E-05
<i>glpC</i>	anaerobi	4.11824	0.000869
<i>glpT</i>	sn-glyce	2.47999	0.006683
<i>glsB</i>	glutamin	2.36569	0.004875
<i>glyA</i>	serine h	3.80796	0.000444
<i>gnsA</i>	putative	2.63495	0.004356
<i>gsk</i>	inosine/	4.80809	0.00054
<i>gspC</i>	Type II	1.85125	0.020354
<i>gspL</i>	Type II	3.06048	0.001622
<i>gudD</i>	D-glucar	3.19298	0.002558
<i>gutM</i>	DNA-bind	4.37677	0.000505
<i>hcr</i>	NADH oxi	3.48981	0.001403
<i>hdeD</i>	acid-res	1.78394	0.025241
<i>hdhA</i>	7-alpha-	2.24626	0.00514
<i>hha</i>	hemolysi	2.53505	0.005315
<i>hinT</i>	purine n	3.69142	0.000866
<i>hipA</i>	serine/t	1.83327	0.02744
<i>hisG</i>	ATP phos	1.74319	0.036255
<i>holE</i>	DNA poly	2.39872	0.009799
<i>hprS</i>	sensory	2.61356	0.004957
<i>hscC</i>	chaperon	3.99411	0.000319
<i>hsdR</i>	type I r	3.51326	0.001076
<i>hupB</i>	DNA-bind	1.95964	0.014522
<i>hyaA</i>	hydrogen	4.54402	0.000336
<i>hyfD</i>	hydrogen	3.27905	0.001268
<i>hyi</i>	hydroxyp	2.97323	0.002878
<i>idnK</i>	D-glucon	4.8864	0.000246
<i>idnO</i>	5-keto-D	4.22093	0.000407
<i>inaA</i>	putative	1.7063	0.037453

<i>insD-3</i>	CP4-44 p	3.55582	0.000755
<i>insG</i>	KpLE2 ph	3.27568	0.001066
<i>insJ</i>	insertio	3.19649	0.00186
<i>insQ</i>	putative	3.14375	0.001792
<i>intD</i>	DLP12 pr	2.22782	0.012958
<i>intQ</i>	EcoGene:	2.29266	0.008038
<i>ivy</i>	periplas	2.39657	0.009359
<i>katE</i>	catalase	3.33436	0.002529
<i>kduD</i>	putative	2.13233	0.019715
<i>kefC</i>	K(+): H	3.69459	0.000955
<i>kgtP</i>	alpha-ke	2.16689	0.011347
<i>kptA</i>	RNA 2'-p	2.80717	0.001462
<i>kup</i>	K(+):H(+	3.40542	0.00224
<i>lacA</i>	galactos	3.99187	0.000867
<i>lapB</i>	lipopoly	2.25161	0.006516
<i>ldcC</i>	lysine d	2.72648	0.002275
<i>leuE</i>	leucine	2.79497	0.005382
<i>leuO</i>	DNA-bind	3.36947	0.003686
<i>leuX</i>	EcoGene:	3.25435	0.001623
<i>lgoD</i>	L-galact	3.83636	0.000705
<i>ligB</i>	DNA liga	3.82787	0.000311
<i>lplA</i>	lipoate-	3.13771	0.001553
<i>lptG</i>	lipopoly	2.30252	0.010983
<i>lpdT</i>	Kdo2-lip	2.56442	0.003247
<i>lsrB</i>	Autoindu	3.5847	0.001427
<i>lsrF</i>	3-hydrox	2.97408	0.002566
<i>lysO</i>	L-lysine	4.00853	0.000696
<i>maeA</i>	malate d	3.28258	0.001035
<i>malK</i>	maltose	2.55352	0.005871
<i>malT</i>	DNA-bind	3.91482	0.000522
<i>marA</i>	DNA-bind	3.56076	0.001286
<i>mazG</i>	nucleosi	2.3202	0.00734
<i>mcrB</i>	5-methyl	2.56304	0.007444
<i>mdfA</i>	multidru	2.39343	0.007827
<i>mdtF</i>	multidru	2.82678	0.003061
<i>mdtI</i>	multidru	3.45867	0.0012
<i>melB</i>	melibios	3.09716	0.002141
<i>mepH</i>	peptidog	3.85695	0.000523
<i>mepS</i>	peptidog	3.20293	0.000684
<i>metF</i>	5,10-met	2.88345	0.002622
<i>mglB</i>	D-galact	3.88476	0.000576
<i>mglC</i>	D-galact	3.79361	0.000465
<i>mgtA</i>	Mg(2+))	4.6814	0.000306
<i>mhpT</i>	3-hydrox	2.12408	0.018052
<i>mioC</i>	flavopro	3.15141	0.000741

<i>mlc</i>	DNA-bind	3.19718	0.002274
<i>mnmA</i>	tRNA-spe	2.03552	0.014036
<i>mntR</i>	DNA-bind	3.72348	0.000632
<i>mocA</i>	molybden	2.18139	0.011053
<i>mqSA</i>	antitoxi	1.94406	0.03866
<i>mrr</i>	methylat	2.5297	0.009857
<i>murB</i>	UDP-N-ac	5.23451	0.000113
<i>murJ</i>	putative	4.33023	0.000451
<i>mutH</i>	DNA mism	2.81254	0.003705
<i>mutS</i>	DNA mism	2.551	0.004364
<i>nadE</i>	NAD synt	2.99299	0.001341
<i>nagE</i>	N-acetyl	2.4456	0.00484
<i>nanS</i>	N-acetyl	2.23442	0.016123
<i>narU</i>	nitrate/	3.51269	0.000744
<i>narV</i>	nitrate	2.29826	0.013573
<i>nei</i>	endonucl	2.20728	0.008705
<i>nfsB</i>	NAD(P)H	3.98317	0.000391
<i>nhoA</i>	arylamin	2.24048	0.008005
<i>nimR</i>	DNA-bind	4.12272	0.000548
<i>nlpE</i>	lipoprot	3.3203	0.000826
<i>nrfA</i>	cytochro	3.35355	0.001978
<i>nth</i>	endonucl	4.00807	0.000456
<i>nudC</i>	NADH pyr	2.17209	0.014075
<i>nudI</i>	pyrimidi	2.50241	0.004864
<i>nupG</i>	nucleosi	3.52195	0.001802
<i>ompL</i>	putative	3.05946	0.00223
<i>ompW</i>	outer me	3.35143	0.000801
<i>omrA</i>		3.28303	0.000849
<i>opgG</i>	osmoregu	3.03265	0.003698
<i>oppA</i>	oligopep	2.17627	0.008743
<i>oppB</i>	murein t	2.66589	0.006473
<i>oppF</i>	murein t	3.2729	0.001644
<i>osmY</i>	periplas	2.08277	0.013098
<i>otsA</i>	trehalos	2.34588	0.009072
<i>otsB</i>	trehalos	3.82569	0.000456
<i>pagP</i>	Lipid IV	2.63611	0.003879
<i>patD</i>	gamma-am	2.51373	0.006787
<i>pdeA</i>	putative	3.1388	0.002298
<i>pdeC</i>	c-di-GMP	2.78455	0.002362
<i>pdeG</i>	putative	3.22888	0.001687
<i>pdeI</i>	putative	4.13584	0.0005
<i>pdxI</i>	pyridoxi	2.64872	0.003089
<i>pfkB</i>	6-phosph	5.95236	4.29E-05
<i>pgaA</i>	partiall	2.64082	0.003284
<i>pgaC</i>	poly-N-a	3.31088	0.001266

<i>pgaD</i>	poly-N-a	3.28279	0.00094
<i>pgpB</i>	phosphat	4.4898	0.000471
<i>pgrR</i>	DNA-bind	2.72683	0.003104
<i>phoE</i>	outer me	2.77467	0.003874
<i>phoR</i>	sensory	2.87587	0.003837
<i>phr</i>	deoxyrib	2.6502	0.004361
<i>plaP</i>	putresci	2.9611	0.001127
<i>plsY</i>	putative	5.74664	0.000123
<i>pnuC</i>	nicotina	3.75346	0.000834
<i>ppiB</i>	peptidyl	2.43207	0.009286
<i>pqiA</i>	intermem	2.87167	0.004811
<i>pqqL</i>	putative	2.78079	0.003428
<i>preA</i>	NAD-depe	2.01713	0.019529
<i>prkB</i>	putative	2.28181	0.010895
<i>prlF</i>	antitoxi	3.58466	0.001249
<i>proP</i>	osmolyte	2.86009	0.004358
<i>proY</i>	putative	4.11058	0.00053
<i>psd</i>	phosphat	6.61404	0.000175
<i>pspA</i>	phage sh	3.23177	0.001068
<i>pspE</i>	thiosulf	2.4833	0.005857
<i>psuG</i>	pseudour	3.48637	0.001888
<i>psuT</i>	putative	2.70779	0.005987
<i>purF</i>	amidopho	3.90306	0.000833
<i>purH</i>	bifuncti	4.61519	0.000222
<i>pyrF</i>	orotidin	1.98051	0.024167
<i>qseC</i>	sensory	5.24953	0.000126
<i>queD</i>	6-carbox	3.91795	0.00044
<i>ralA</i>	EcoGene:	2.87159	0.00321
<i>rapZ</i>	RNase ad	3.4077	0.001156
<i>rbn</i>	ribonucl	6.15999	9.97E-05
<i>rcdA</i>	DNA-bind	3.62215	0.000653
<i>rclA</i>	putative	2.22594	0.010566
<i>rclR</i>	DNA-bind	2.24198	0.008997
<i>rcsC</i>	sensory	2.12031	0.017296
<i>rhmD</i>	L-rhamno	4.96733	0.00023
<i>rhsA</i>	rhs elem	2.67375	0.003906
<i>rhsB</i>	rhs elem	3.26683	0.0006
<i>rhsC</i>	rhs elem	4.34693	0.000534
<i>rhsD</i>	protein	4.91196	0.0002
<i>rhsE</i>	EcoGene:	2.91494	0.002578
<i>rimK</i>	ribosoma	3.07653	0.00191
<i>rimL</i>	ribosoma	2.88055	0.002023
<i>rlhA</i>	23S rRNA	2.7037	0.008025
<i>rlmB</i>	23S rRNA	3.81362	0.000814
<i>rng</i>	RNase G	2.97008	0.002521

<i>rpiB</i>	alloose-6	3.81836	0.000766
<i>rpnB</i>	recombin	2.87497	0.003594
<i>rpnC</i>	recombin	2.2148	0.018134
<i>rpnD</i>	EcoGene:	2.14164	0.013103
<i>rpsJ</i>	30S ribo	4.18869	0.000746
<i>rraB</i>	ribonucl	3.56034	0.001452
<i>rspB</i>	putative	3.0562	0.001467
<i>rssA</i>	putative	6.15757	4.83E-05
<i>rssB</i>	regulato	1.95462	0.014175
<i>rtcB</i>	RNA-spli	4.74327	0.000225
<i>rybA</i>		6.45678	0.000155
<i>sapD</i>	putresci	2.95145	0.004519
<i>sbmA</i>	peptide	2.15825	0.015261
<i>scpB</i>	methylma	1.84282	0.037437
<i>sdhC</i>	succinat	2.01387	0.015101
<i>setC</i>	putative	2.50538	0.007359
<i>sfmC</i>	putative	4.12312	0.000194
<i>sfmD</i>	putative	3.19718	0.002274
<i>sfsB</i>	putative	3.2539	0.001033
<i>shiA</i>	shikimat	2.08937	0.011204
<i>sieB</i>	Rac prop	5.03026	0.00035
<i>slp</i>	starvati	3.38241	0.00158
<i>smf</i>	protein	3.50439	0.001094
<i>sodA</i>	superoxi	2.09705	0.007582
<i>sohB</i>	S49 pept	2.86765	0.00199
<i>soxR</i>	DNA-bind	2.01594	0.01786
<i>speF</i>	ornithin	2.42642	0.006401
<i>speG</i>	spermidi	3.01657	0.000864
<i>srlA</i>	sorbitol	3.063	0.001748
<i>sseA</i>	3-mercap	2.3313	0.005644
<i>tag</i>	3-methyl	3.64747	0.001033
<i>talA</i>	transald	2.6987	0.003712
<i>tamA</i>	transloc	2.04756	0.013563
<i>tar</i>	methyl-a	3.24284	0.001068
<i>tdcE</i>	2-ketobu	3.09253	0.001475
<i>tdcR</i>	DNA-bind	2.79554	0.004574
<i>tehA</i>	tellurit	3.83597	0.000199
<i>tgt</i>	tRNA-gua	4.29385	0.00063
<i>thiI</i>	tRNA uri	3.20155	0.001464
<i>tktB</i>	transket	2.43768	0.007453
<i>tnaA</i>	tryptoph	3.05191	0.002287
<i>tonB</i>	Ton comp	2.59089	0.008793
<i>torT</i>	periplas	2.76964	0.002405
<i>treA</i>	periplas	2.57815	0.005322
<i>treF</i>	cytoplas	2.66149	0.005414

<i>trkG</i>	Rac prop	2.77487	0.003659
<i>trmA</i>	tRNA m(5	3.44856	0.000879
<i>tsgA</i>	putative	3.43966	0.001517
<i>tsr</i>	methyl-a	4.01993	0.000456
<i>ttcC</i>	EcoGene:	2.3581	0.007955
<i>tynA</i>	copper-c	3.13056	0.00081
<i>tyrB</i>	tyrosine	2.5615	0.015441
<i>tyrP</i>	tyrosine	4.62469	0.000249
<i>uacT</i>	urate:H(3.78689	0.000848
<i>ubiG</i>	bifuncti	3.00905	0.001453
<i>ubiK</i>	ubiquino	2.56497	0.004441
<i>ucpA</i>	putative	3.58325	0.000992
<i>ugd</i>	UDP-gluc	2.74641	0.003862
<i>ugpB</i>	sn-glyce	3.33416	0.001397
<i>uidA</i>	beta-glu	2.66597	0.003238
<i>uidC</i>	outer me	2.44501	0.00846
<i>ulaR</i>	DNA-bind	3.04758	0.001662
<i>umuC</i>	DNA poly	2.98827	0.001183
<i>ung</i>	uracil-D	2.89322	0.00361
<i>upp</i>	uracil p	3.33983	0.000712
<i>ushA</i>	5'-nucle	3.40939	0.00088
<i>uvrB</i>	excision	2.14442	0.015261
<i>ves</i>	HutD fam	2.77175	0.002219
<i>wcaA</i>	putative	3.69764	0.00103
<i>wcaE</i>	putative	3.76881	0.000814
<i>wecH</i>	O-acetyl	2.08117	0.019825
<i>wza</i>	outer me	3.13543	0.001316
<i>wzzB</i>	regulato	2.17309	0.013769
<i>xanQ</i>	xanthine	3.41631	0.000939
<i>xdhC</i>	putative	2.18533	0.007547
<i>xseA</i>	exodeoxy	2.75795	0.004798
<i>xthA</i>	exodeoxy	3.78206	0.000989
<i>xylF</i>	xylose A	3.86907	0.000859
<i>xylH</i>	xylose A	2.62649	0.005546
<i>xylR</i>	DNA-bind	2.24278	0.009004
<i>yaaU</i>	putative	6.97264	0.000186
<i>yadG</i>	putative	2.49027	0.006436
<i>yadH</i>	putative	6.95438	3.85E-05
<i>yadM</i>	putative	2.45536	0.006509
<i>yadV</i>	putative	3.55219	0.001078
<i>yafN</i>	antitoxi	2.46402	0.002794
<i>yafT</i>	lipoprot	4.44276	0.000407
<i>yagU</i>	inner me	3.94266	0.000475
<i>yahD</i>	ankyrin	7.41019	1.71E-05
<i>yahJ</i>	putative	2.5358	0.004461

<i>yahO</i>	DUF1471	2.36403	0.01313
<i>yaiZ</i>	DUF2754	3.92317	0.000276
<i>ybaL</i>	putative	9.59544	2.58E-05
<i>ybaQ</i>	putative	3.47356	0.001005
<i>ybaV</i>	helix-ha	3.5731	0.001019
<i>ybbP</i>	putative	2.66867	0.005122
<i>ybbW</i>	putative	4.76308	0.000132
<i>ybcL</i>	DLP12 pr	3.51187	0.000971
<i>ybcW</i>	DLP12 pr	2.03155	0.019642
<i>ybdG</i>	minicond	3.53188	0.001094
<i>ybdK</i>	carboxyl	2.85198	0.004026
<i>ybdR</i>	putative	2.21635	0.010534
<i>ybeD</i>	DUF493 d	2.00079	0.009804
<i>ybeF</i>	putative	3.17329	0.001867
<i>ybeL</i>	DUF1451	1.88971	0.039902
<i>ybfL</i>	EcoGene:	2.47781	0.005246
<i>ybfO</i>	EcoGene:	2.13937	0.010612
<i>ybfP</i>	lipoprot	4.17871	0.0004
<i>ybjI</i>	5-amino-	2.90529	0.002032
<i>ybjM</i>	putative	3.21655	0.000962
<i>ycaK</i>	putative	2.63074	0.004056
<i>ycbU</i>	putative	2.14057	0.009631
<i>yccU</i>	putative	3.02474	0.001739
<i>ycdX</i>	zinc-bin	2.58304	0.002878
<i>ycdZ</i>	putative	3.17246	0.002004
<i>yceJ</i>	putative	2.92188	0.001761
<i>yceK</i>	DUF1375	3.3895	0.001293
<i>yceQ</i>	DUF2655	4.78352	0.00021
<i>ycfT</i>	inner me	6.07512	0.000684
<i>ycfZ</i>	putative	3.8256	0.000827
<i>ycgH</i>	EcoGene:	2.81869	0.005253
<i>ycgI</i>	EcoGene:	2.43278	0.003602
<i>ycgJ</i>	PF05666	2.9801	0.000887
<i>ycgL</i>	PF05166	3.85364	0.000895
<i>ycgN</i>	PF03693	2.19793	0.008213
<i>ycgV</i>	putative	2.76087	0.003861
<i>ycgX</i>	uncharac	4.7812	0.000154
<i>ycgZ</i>	putative	2.45506	0.006649
<i>yciQ</i>	DUF2207	2.24838	0.012458
<i>yciW</i>	putative	3.06492	0.001831
<i>ycjF</i>	conserve	2.6452	0.002911
<i>ycjG</i>	L-Ala-D/	3.2317	0.00155
<i>ycjM</i>	glucosyl	3.72927	0.000668
<i>ycjV</i>	EcoGene:	2.11131	0.010623
<i>ydbD</i>	DUF2773	2.5218	0.006016

<i>ydbH</i>	PF11739	3.29383	0.001801
<i>ydcR</i>	fused pu	3.39211	0.001245
<i>yddW</i>	putative	3.27001	0.001567
<i>ydeA</i>	L-arabin	3.54505	0.000839
<i>ydeE</i>	dipeptid	2.19793	0.008213
<i>ydeO</i>	DNA-bind	2.72187	0.005115
<i>ydeP</i>	putative	2.31244	0.016087
<i>ydeQ</i>	putative	2.434	0.002594
<i>ydfE</i>	EcoGene:	4.76856	0.000487
<i>ydfG</i>	3-hydrox	3.17795	0.001451
<i>ydfI</i>	putative	2.68228	0.002523
<i>ydgA</i>	conserve	2.61903	0.001949
<i>ydhK</i>	putative	2.77487	0.003659
<i>ydhP</i>	putative	3.15226	0.0018
<i>ydhQ</i>	adhesin-	4.04564	0.001065
<i>ydhR</i>	putative	2.92637	0.002012
<i>ydhV</i>	putative	2.79472	0.00312
<i>ydiF</i>	putative	3.36923	0.001141
<i>ydiK</i>	putative	2.16654	0.012166
<i>ydiM</i>	putative	3.09896	0.00131
<i>ydiP</i>	putative	1.98064	0.018528
<i>ydiV</i>	anti-Flh	3.6627	0.00053
<i>ydjE</i>	putative	2.60445	0.004131
<i>ydjF</i>	putative	2.58201	0.004598
<i>ydjG</i>	NADH-dep	2.81792	0.002884
<i>ydjI</i>	putative	2.1403	0.014676
<i>ydjJ</i>	putative	3.54018	0.001039
<i>ydjL</i>	putative	2.81792	0.002884
<i>ydjY</i>	4Fe-4S f	4.18181	0.000371
<i>yeaH</i>	DUF444 d	3.62643	0.001193
<i>yeaV</i>	putative	6.64458	6.52E-05
<i>yebV</i>	protein	4.56427	0.000425
<i>yeeA</i>	putative	2.77485	0.002635
<i>yeeD</i>	putative	2.79844	0.004268
<i>yeeJ</i>	inverse	2.64797	0.003818
<i>yeeN</i>	putative	3.21816	0.001443
<i>yeeX</i>	DUF496 d	2.03919	0.010223
<i>yegH</i>	inner me	3.61657	0.000589
<i>yegS</i>	lipid ki	2.71126	0.004454
<i>yehR</i>	DUF1307	3.68315	0.00065
<i>yehS</i>	conserve	2.08162	0.015914
<i>yeiG</i>	S-formyl	3.60651	0.000386
<i>yeiL</i>	putative	3.55019	0.001102
<i>yeiS</i>	DUF2542	2.90474	0.001877
<i>yejA</i>	putative	6.1914	8.01E-05

<i>yejE</i>	putative	3.32037	0.002543
<i>yejF</i>	putative	3.27427	0.000998
<i>yejM</i>	putative	3.54813	0.000272
<i>yfaA</i>	DUF2138	5.31562	9.43E-05
<i>yfaL</i>	putative	3.37515	0.001288
<i>yfaQ</i>	tandem D	4.16266	0.000562
<i>yfaZ</i>	putative	2.75624	0.003522
<i>yfcV</i>	putative	2.50062	0.00351
<i>yfdV</i>	putative	4.23989	0.000488
<i>yfdX</i>	protein	2.64961	0.002402
<i>yfeC</i>	putative	5.6406	0.00011
<i>yfeH</i>	putative	3.35451	0.001517
<i>yfeS</i>	conserve	2.04393	0.017766
<i>yfgG</i>	protein	2.85672	0.001435
<i>yfiE</i>	putative	4.05255	0.000368
<i>ygbE</i>	conserve	4.51869	0.000413
<i>ygcE</i>	putative	3.01677	0.002447
<i>ygdG</i>	flap end	2.99763	0.001815
<i>ygdQ</i>	UPF0053	3.45008	0.000532
<i>ygeR</i>	LysM dom	2.92859	0.005268
<i>ygeV</i>	putative	3.80939	0.000745
<i>ygeW</i>	putative	3.55642	0.001877
<i>ygfI</i>	putative	3.32481	0.001343
<i>ygfK</i>	putative	2.32429	0.013677
<i>ygZ</i>	folate-b	2.63917	0.007427
<i>yggM</i>	DUF1202	3.33072	0.001801
<i>yggP</i>	putative	4.89741	0.000152
<i>yggT</i>	uncharac	3.07368	0.003569
<i>yghG</i>	lipoprot	4.25311	0.000161
<i>yghO</i>	putative	2.47519	0.007884
<i>yghQ</i>	putative	1.88233	0.011884
<i>ygiC</i>	putative	2.41613	0.008853
<i>ygiI</i>	putative	3.39297	0.001651
<i>ygjP</i>	putative	2.29951	0.005966
<i>yhaH</i>	putative	2.50771	0.006408
<i>yhcB</i>	conserve	2.45846	0.004127
<i>yhdJ</i>	DNA aden	3.21335	0.001732
<i>yhdU</i>	DUF2556	3.14483	0.00195
<i>yhdZ</i>	putative	2.90849	0.005984
<i>yhfL</i>	DUF4223	3.34734	0.001003
<i>yhfW</i>	putative	2.68064	0.004364
<i>yhgH</i>	DNA util	4.30313	0.000192
<i>yhhT</i>	putative	2.31043	0.009637
<i>yhhX</i>	putative	3.03606	0.001768
<i>yhhY</i>	N-acetyl	2.82632	0.001954

<i>yhiJ</i>	DUF4049	2.48093	0.006391
<i>yhjD</i>	putative	2.47451	0.006189
<i>yhjG</i>	AsmA fam	3.42274	0.000756
<i>yhjV</i>	putative	6.70431	9.67E-05
<i>yiaK</i>	2,3-dike	3.36778	0.001966
<i>yiaN</i>	2,3-dike	3.12656	0.001006
<i>yiaY</i>	L-threon	3.11928	0.00171
<i>yibJ</i>	EcoGene:	2.5425	0.008925
<i>yicH</i>	AsmA fam	2.47472	0.008081
<i>yicJ</i>	putative	3.56727	0.00128
<i>yicN</i>	conserve	2.50241	0.004864
<i>yicS</i>	uncharac	4.48239	0.000301
<i>yidE</i>	putative	2.97367	0.002715
<i>yidI</i>	putative	3.49878	0.00094
<i>yidL</i>	putative	3.03331	0.004586
<i>yidP</i>	putative	4.16598	0.001063
<i>yidX</i>	putative	4.02963	0.000407
<i>yidZ</i>	putative	2.63835	0.004259
<i>yifN</i>	EcoGene:	2.91433	0.003186
<i>yigE</i>	DUF2233	2.67273	0.004997
<i>yihN</i>	putative	2.9491	0.002776
<i>yihR</i>	putative	2.62312	0.004706
<i>yihW</i>	putative	3.49843	0.00101
<i>yiiE</i>	putative	3.59039	0.00093
<i>yiiG</i>	DUF3829	2.58217	0.001683
<i>yiiQ</i>	DUF1454	2.90208	0.001397
<i>yiiR</i>	DUF805 d	3.38256	0.000756
<i>yijE</i>	cystine	4.18359	0.000544
<i>yijF</i>	conserve	4.38107	0.00016
<i>yjaG</i>	conserve	2.81668	0.001741
<i>yjaZ</i>	conserve	3.36615	0.002075
<i>yjbD</i>	conserve	2.3954	0.005977
<i>yjbH</i>	YjbH fam	5.8791	0.000198
<i>yjbI</i>	EcoGene:	2.77294	0.003386
<i>yjbJ</i>	putative	3.77683	0.000455
<i>yjdI</i>	PF06902	4.57505	0.000251
<i>yjdM</i>	conserve	2.9752	0.002186
<i>yjeM</i>	putative	4.5984	0.000398
<i>yjeV</i>	uncharac	2.71122	0.00456
<i>yjgN</i>	conserve	3.81835	0.000664
<i>yjgX</i>	EcoGene:	3.031	0.002335
<i>yjhB</i>	putative	2.79463	0.003428
<i>yjhR</i>	EcoGene:	4.12021	0.000662
<i>yjhZ</i>	EcoGene:	2.9207	0.000265
<i>yjiK</i>	uncharac	4.10718	0.001232

<i>yjiM</i>	putative		2.86133	0.001562
<i>yjiV</i>	EcoGene:		3.0817	0.002621
<i>yjjB</i>	putative		3.4033	0.000589
<i>yjjQ</i>	DNA-bind		4.38273	0.000417
<i>ykgA</i>	EcoGene:		3.49504	0.000461
<i>ykgE</i>	putative		2.50241	0.004864
<i>ykgG</i>		#N/A	2.8606	0.002597
<i>ykgL</i>	uncharac		4.09417	0.00045
<i>ykgP</i>	EcoGene:		2.5309	0.003151
<i>ylaC</i>	putative		2.75113	0.002758
<i>ylcG</i>	DLP12 pr		2.6828	0.004012
<i>yliI</i>	aldose s		3.2525	0.001681
<i>ymdG</i>	protein		3.94288	0.000384
<i>ymgE</i>	PF04226		2.88381	0.001886
<i>yngM</i>	protein		3.24767	0.000932
<i>ymiA</i>	uncharac		3.01941	0.001337
<i>ymjC</i>	putative		5.07462	0.000298
<i>ynbC</i>	hydrolas		2.76299	0.002635
<i>yncE</i>	PQQ-like		2.28666	0.022358
<i>yncG</i>	putative		3.6268	0.000824
<i>yneK</i>	protein		4.67481	0.00022
<i>yneO</i>	EcoGene:		3.30369	0.001922
<i>yneP</i>	protein		2.7332	0.002923
<i>ynfA</i>	conserve		3.62576	0.000505
<i>ynfE</i>	putative		2.35721	0.005207
<i>ynfF</i>	putative		3.24001	0.001821
<i>yniA</i>	putative		3.21683	0.00211
<i>ynjI</i>	DUF1266		3.12589	0.002614
<i>yohJ</i>	PF03788		2.20389	0.010534
<i>ypdI</i>	colanic		2.26495	0.011241
<i>ypfN</i>	UPF0370		2.45846	0.004127
<i>yphF</i>	putative		5.35076	0.000163
<i>yqcE</i>	putative		2.40951	0.007147
<i>yqcG</i>	cell env		4.81087	0.00017
<i>yqeA</i>	putative		2.7201	0.00193
<i>yqeG</i>	putative		4.01743	0.000912
<i>yqeH</i>		#N/A	2.41641	0.003586
<i>yqhA</i>	uncharac		2.84179	0.001619
<i>yqiH</i>	putative		2.12153	0.019122
<i>yraI</i>	putative		2.35815	0.014839
<i>yraJ</i>	putative		3.39808	0.001326
<i>yraK</i>	putative		2.59243	0.004279
<i>yrda</i>	protein		3.56932	0.000588
<i>yrdD</i>	putative		3.94701	0.000545
<i>yrhD</i>	uncharac		12.03588	6.44E-06

<i>ysdD</i>	protein	5.08069	0.000185
<i>zapC</i>	cell div	2.18883	0.012116
<i>zinT</i>	metal-bi	2.14845	0.008027
<i>zitB</i>	Zn(2(+))	4.24332	0.000253
<i>zntB</i>	Zn(2(+))	5.69192	0.000158
<i>aaeR</i>	LysR-typ	3.15807	0.00127
<i>acnA</i>	aconitat	2.37116	0.005175
<i>acrF</i>	multidru	5.47303	0.000176
<i>aidB</i>	putative	6.13982	7.4E-05
<i>arnT</i>	lipid IV	3.72316	0.001272
<i>atoC</i>	DNA-bind	2.32875	0.008729
<i>dgcE</i>	putative	3.81112	0.000476
<i>dosP</i>	oxygen-s	7.02668	4.24E-05
<i>katE</i>	catalase	3.07545	0.00168
<i>ompW</i>	outer me	2.96956	0.00347
<i>pdeI</i>	putative	4.11056	0.000615
<i>pdeI</i>	putative	3.36731	0.00158
<i>pqqL</i>	putative	6.89165	0.001264
<i>rbn</i>	ribonucl	2.55844	0.000926
<i>sfdM</i>	putative	3.31242	0.0014
<i>sohB</i>	S49 pept	2.66602	0.002279
<i>tehA</i>	tellurit	2.3202	0.00734
<i>tktB</i>	transket	2.34083	0.004759
<i>treF</i>	cytoplas	3.28943	0.001072
<i>tsgA</i>	putative	4.15513	0.00056
<i>ybdR</i>	putative	5.01687	0.00019
<i>ycgV</i>	putative	2.24195	0.010447
<i>ydeE</i>	dipeptid	4.10551	0.000536
<i>yeaV</i>	putative	2.11507	0.002093
<i>yeeJ</i>	inverse	2.50304	0.005352
<i>ygeR</i>	LysM dom	3.13815	0.001332
<i>yjhR</i>	EcoGene:	2.85879	0.001632
<i>zntB</i>	Zn(2(+))	4.37755	0.000382

Supplementary Table 7. Bacterial strains used in this study

Strain	Relevant characteristic(s)	Reference or source
<i>B. coagulans</i> 2-6	Wild type	ref. 22
<i>E. coli</i> DH5α	<i>supE44ΔlacU169</i> ($\Phi 80$ <i>lacZΔM15</i>) <i>hsdR17 recA1 endA1 gyrA96 thi-1</i> <i>relA1</i>	Novagen
<i>E. coli</i> BL21 (DE3)	<i>F-</i> <i>ompT hsdSB (rB-mB-) gal (λ c I 857 ind1 Sam7 nin5 lacUV5 T7gene1) dcm (DE3)</i>	Novagen
<i>P. putida</i> KT2440	<i>rmo- mod+</i>	ATCC
<i>S. cerevisiae</i> INVSc1	<i>MATa his3D1 leu2 trp1-289 ura3-52</i> <i>MAT his3D1 leu2 trp1-289 ura3-52</i>	ATCC
ATCC31280::pLQ856	wild-type harboring pLQ856	Ning, Wang <i>et al.</i> , 2017
ATCC31280::pLQ856- <i>cspL</i>	wild-type harboring pLQ856- <i>cspL</i>	This study
DH5α	<i>E. coli</i> DH5α harboring pUC19 empty vector	This study
DH5α- <i>cspL</i>	<i>E. coli</i> DH5α harboring pUC19- <i>cspL</i>	This study
DH5α- <i>cspD</i>	<i>E. coli</i> DH5α harboring pUC19- <i>cspD</i>	This study
DH5α- <i>BCO26_YkuS</i>	<i>E. coli</i> DH5α harboring pUC19- <i>BCO26_ykuS</i>	This study
DH5α- <i>BCO26_2915</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_2915</i>	This study
DH5α- <i>BCO26_Dps</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_dps</i>	This study
DH5α- <i>BCO26_GsiB</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_gsiB</i>	This study
DH5α- <i>BCO26_YbfB</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_ybfB</i>	This study
DH5α- <i>BCO26_MntH</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_mntH</i>	This study
DH5α- <i>BCO26_2932</i>	<i>E. coli</i> DH5α harboring pUC19 <i>BCO26_2932</i>	This study
DH5α- <i>BCO26_GabD</i>	<i>E. coli</i> DH5α harboring	This study

	pUC19BCO26_gabD	
DH5α-BCO26_GroEL	<i>E. coli</i> DH5α harboring pUC19BCO26_groEL	This study
DH5α-BCO26_HrcA	<i>E. coli</i> DH5α harboring pUC19BCO26_hrcA	This study
DH5α-BCO26_ClpE	<i>E. coli</i> DH5α harboring pUC19BCO26_clpE	This study
DH5α-BCO26_1771	<i>E. coli</i> DH5α harboring pUC19BCO26_1771	This study
DH5α-BCO26_DnaK	<i>E. coli</i> DH5α harboring pUC19BCO26_dnaK	This study
DH5α-BCO26_GroES	<i>E. coli</i> DH5α harboring pUC19BCO26_groES	This study
DH5α-BCO26_0541	<i>E. coli</i> DH5α harboring pUC19BCO26_0541	This study
DH5α-BCO26_YkzI	<i>E. coli</i> DH5α harboring pUC19BCO26_ykzI	This study
DH5α-BCO26_KatE	<i>E. coli</i> DH5α harboring pUC19BCO26_katE	This study
DH5α-BCO26_0399	<i>E. coli</i> DH5α harboring pUC19BCO26_0399	This study
DH5α-BCO26_2461	<i>E. coli</i> DH5α harboring pUC19BCO26_2461	This study
DH5α-BCO26_LevG	<i>E. coli</i> DH5α harboring pUC19BCO26_levG	This study
DH5α-BCO26_YqiG	<i>E. coli</i> DH5α harboring pUC19BCO26_yqiG	This study
DH5α-BCO26_2340	<i>E. coli</i> DH5α harboring pUC19BCO26_2340	This study
DH5α-BCO26_YfIT	<i>E. coli</i> DH5α harboring pUC19BCO26_yfIT	This study
DH5α-BCO26_ArgI	<i>E. coli</i> DH5α harboring pUC19BCO26_argI	This study
DH5α-BCO26_SucC	<i>E. coli</i> DH5α harboring pUC19BCO26_sucC	This study
DH5α-BCO26_2370	<i>E. coli</i> DH5α harboring pUC19BCO26_2370	This study
DH5α-BCO26_CitZ	<i>E. coli</i> DH5α harboring pUC19BCO26_citZ	This study
DH5α-BCO26_RsbV	<i>E. coli</i> DH5α harboring	This study

	pUC19BCO26_rsbV	
DH5α-BCO26_Hag	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_rhag	
DH5α-BCO26_YhgD	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_yhgD	
DH5α-BCO26_1679	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_1679	
DH5α-BCO26_RsbW	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_rsbW	
DH5α-BCO26_YteA	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_yteA	
DH5α-BCO26_2825	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_2825	
DH5α-BCO26_LevE	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_levE	
DH5α-BCO26_SigB	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_sigB	
DH5α-BCO26_2573	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_2573	
DH5α-BCO26_1484	<i>E. coli</i> DH5α harboring	This study
	pUC19BCO26_1484	
BL21-cspL	<i>E. coli</i> BL21(DE3) harboring	This study
	pET28a-cspL	
BL21-cspL-M11	<i>E. coli</i> BL21(DE3) harboring	This study
	pET28a-cspL with mutated	
	G14 Y15 G16 F17 I18 E19 R20	
	V26 F27 V28 H29	
BL21-cspL-M7	<i>E. coli</i> BL21(DE3) harboring	This study
	pET28a-cspL with mutated	
	G14 Y15 G16 F17 I18 E19 R20	
INVSc1	<i>S. cerevisiae</i> INVSc1 harboring	This study
	pYES2 empty vector	
INVSc1-cspL	<i>S. cerevisiae</i> INVSc1 harboring	This study
	pYES2-cspL	
KT2440	<i>P. putida</i> KT2440 harboring	This study
	pME6032 empty vector	
KT2440-cspL	<i>P. putida</i> KT2440 harboring	This study
	pME6032-cspL	
DH5α-cspA	<i>E. coli</i> DH5α harboring pUC19-cspA	This study

Supplementary Table 8. Plasmids used in this study

Plasmid	Relevant characteristic(s) ^a	Reference or source
pUC19	Amp ^R , <i>pMB1 ori, PlacZ</i>	Novagen
pET28a(+)	Kan ^R , <i>pBR322 ori, PT7</i>	Novagen
pUC19- <i>cspL</i>	pUC19 harboring <i>cspL</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_cspD</i>	pUC19 harboring <i>BCO26_cspD</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_ykuS</i>	pUC19 harboring <i>BCO26_ykuS</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_2915</i>	pUC19 harboring <i>BCO26_2915</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_dps</i>	pUC19 harboring <i>BCO26_dps</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_gsiB</i>	pUC19 harboring <i>BCO26_gsiB</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_ybfB</i>	pUC19 harboring <i>BCO26_ybfB</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_mntH</i>	pUC19 harboring <i>BCO26_mntH</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_2932</i>	pUC19 harboring <i>BCO26_2932</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO2_gabD</i>	pUC19 harboring <i>BCO2_gabD</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO2_groEL</i>	pUC19 harboring <i>BCO26_groEL</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_hrcA</i>	pUC19 harboring <i>BCO26_hrcA</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_clpE</i>	pUC19 harboring <i>BCO26_clpE</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_1771</i>	pUC19 harboring <i>BCO26_1771</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_dnaK</i>	pUC19 harboring <i>BCO26_dnaK</i> from <i>B. coagulans</i> 2-6	This study
pUC19- <i>BCO26_groES</i>	pUC19 harboring <i>BCO26_groES</i> from	This study

	<i>B. coagulans</i> 2-6	
pUC19-BCO26_0541	pUC19 harboring <i>BCO26_0541</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_ykzI	pUC19 harboring <i>BCO26_ykzI</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_katE	pUC19 harboring <i>BCO26_katE</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_0399	pUC19 harboring <i>BCO26_0399</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_2461	pUC19 harboring <i>BCO26_2461</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_levG	pUC19 harboring <i>BCO26_levG</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_yqiG	pUC19 harboring <i>BCO26_yqiG</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_2340	pUC19 harboring <i>BCO26_2340</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_yfIT	pUC19 harboring <i>BCO26_yfIT</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_argI	pUC19 harboring <i>BCO26_argI</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_sucC	pUC19 harboring <i>BCO26_sucC</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_2370	pUC19 harboring <i>BCO26_2370</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_citZ	pUC19 harboring <i>BCO26_citZ</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_rsbV	pUC19 harboring <i>BCO26_rsbV</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_hag	pUC19 harboring <i>BCO26_hag</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_yhgD	pUC19 harboring <i>BCO26_yhgD</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_1679	pUC19 harboring <i>BCO26_1679</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_rsbW	pUC19 harboring <i>BCO26_rsbW</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_yteA	pUC19 harboring <i>BCO26_yteA</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_2825	pUC19 harboring <i>BCO26_2825</i> from	This study

	<i>B. coagulans</i> 2-6	
pUC19-BCO26_levE	pUC19 harboring <i>BCO26_levE</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_sigB	pUC19 harboring <i>BCO26_sigB</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_2573	pUC19 harboring <i>BCO26_2573</i> from <i>B. coagulans</i> 2-6	This study
pUC19-BCO26_1484	pUC19 harboring <i>BCO26_1484</i> from <i>B. coagulans</i> 2-6	This study
pET28a-cspL	pET28a harboring <i>BCO26_cspL</i> from <i>B. coagulans</i> 2-6	This study
pET28a-cspL-M11	pET-28a harboring <i>BCO26_cspL</i> from <i>B. coagulans</i> 2-6 with mutated G14 Y15 G16 F17 I18 E19 R20 V26 F27 V28 H29	This study
pET28a-cspL-M7	pET-28a harboring <i>BCO26_cspL</i> from <i>B. coagulans</i> 2-6 with mutated G14 Y15 G16 F17 I18 E19 R20	This study
pYES2-cspL	pYES2 harboring <i>BCO26_cspL</i> from <i>B. coagulans</i> 2-6	This study
pME6032-cspL	pME6032 harboring <i>BCO26_cspL</i> from <i>B. coagulans</i> 2-6	Novagen
pUC19-cspA	pUC19 harboring <i>cspA</i> from <i>E. coli</i>	This study
pLQ856	pDR3 derivative	Ning, Wang <i>et</i> <i>al.</i> , 2017
pLQ856-cspL	pLQ856 derivative with inserted <i>cspL</i> under the control of kasOp*	This study

^aAmp^R and Kan^R resistance to ampicillin and kanamycin, respectively.

Supplementary Table 9. Sequences of primers used in this study

Primer	Sequence (5' > 3')
CspL-F	CGCGGATCC atggaacatggtacagtaaa
CspL-R	CCGGAATTCTtagtctttttgaacat
BCO26_CspD-F	CGCGGATCC atgcaaaacggtaaagtaaa
BCO26_CspD-R	CCGGAATTCTtagaaagttttgttacat
BCO26_YkuS-F	CGCGGATCC atggctgtaatcggtgtaga
BCO26_YkuS-R	CCGGAATTCTtacattctgctcgccactt
BCO26_2925-F	CCCAAGCTT atgaaaaagcgggcaattgt
BCO26_2925-R	CGCGGATCC tcaggaaaccactgccttt
BCO26_Dps-F	CGCGGATCC atggcagaaaacgaacaatt
BCO26_Dps-R	CCGGAATTCTtaccgcttccaagaaagg
BCO26_GsiB-F	CCCAAGCTT atggcagacaaagataaaaaa
BCO26_GsiB-R	CGCGGATCC ttaatcttcaccgttgtttt
BCO26_YbfB-F	CGCGGATCC atgttagaacgaaaagcaaa
BCO26_YbfB-R	CCGGAATTCTttaatgcgaatgctggcac
BCO26_MntH-F	CCCAAGCTT atgagtgaaaaaatgtgag
BCO26_MntH-R	CCGGAATTCTttatataaacgttatcaatca
BCO26_2932-F	CCCAAGCTT atgagcatcagacagggaaa
BCO26_2932-R	CGCGGATCC ttaccggtaggccggttctt
BCO26_GabD-F	CGCGGATCC atggaagactatttgatgta
BCO26_GabD-R	CCGGAATTCTttataaaccgagggaaatat
BCO26_GroEL-F	CGCGGATCC atggcaaaagaaattaaatt
BCO26_GroEL-R	CCGGAATTCTttacatcatgcccccattgc
BCO26_HrcA-F	CGCGGATCC atggcggatcttgaggaact
BCO26_HrcA-R	CCGGAATTCTctatctgtcatacaatttcg
BCO26_ClxE-F	CGCGGATCC atgttatgtgacaaatgcca
BCO26_ClxE-R	CCGGAATTCTttattttccgcgtggcaa

BCO26_1771-F	CCCAAGCTT atgtttgatttaatgccatt
BCO26_1771-R	CGCGGATCC ttattgaattcaatccctt
BCO26_DnaK-F	CGCGGATCC atgagcaaattatcgcat
BCO26_DnaK-R	CCGGAATT C ttatttttattatcatcga
BCO26_GroES-F	CGCGGATCC atgttcacgtgtaaaacc
BCO26_GroES-R	CCGGAATT C ttattccacaaccgcagaa
BCO26_0541-F	CGCGGATCC atggtaggaatttattgc
BCO26_0541-R	CCGGAATT C ttattttgttgttcagct
BCO26_YkzI-F	CGCGGATCC atgaaacaagaatcccttc
BCO26_YkzI-R	CCGGAATT C ttacatggcttcatttca
BCO26_KatE-F	CTAGTCTAGA atgagtagtgaacggaaact
BCO26_KatE-R	CGAGCTC tcatatcaa acgcctgtccc
BCO26_0399-F	CCCAAGCTT atgccattggaactggtaat
BCO26_0399-R	CTAGTCTAGA tcaatgcttccccctcta
BCO26_2461-F	CGCGGATCC atgataaaaatcaatggc
BCO26_2461-R	CCGGAATT C tcactttcgcgcctgcaa
BCO26_LevG-F	CCCAAGCTT atggcacaagaactaaatt
BCO26_LevG-R	CTAGTCTAGA ttacattaagtgaattaaat
BCO26_YqiG-F	CGCGGATCC atgagcaaatacgataaact
BCO26_YqiG-R	CCGGAATT C tcactctgcaa acgggaacc
BCO26_2340-F	CCCAAGCTT atgaaccgaaattttgtaa
BCO26_2340-R	CGCGGATCC ttatttcggcactccgca
BCO26_YflT-F	CGCGGATCC atgcataaagttagaagtgg
BCO26_YflT-R	CCGGAATT C ttatagcagggttcaggcc
BCO26_ArgI-F	CGCGGATCC atggagaaacatattgcaat
BCO26_ArgI-R	CCGGAATT C ttaaaagaagttttcccga
BCO26_SucC-F	CGCGGATCC atgaatattc acgagtgatca
BCO26_SucC-R	CCGGAATT C ttagctgaccagttcgacaa
BCO26_2370-F	CGCGGATCC atgagatcgattgtaaatga

BCO26_2370-R	CCGGAAATTCTtaatacagcgtaatttcct
BCO26_CitZ-F	CGCGGATCCatgacagcaacaagaggct
BCO26_CitZ-R	CCGGAAATTCTtaccggcttcgagcggaa
BCO26_RsbV-F	CGCGGATCCatggacttgaagttagatgt
BCO26_RsbV-R	CCGGAAATTCTtcacactccacccttctattt
BCO26_Hag-F	CCCAAGCTTatgattatcaatcacaacat
BCO26_Hag-R	CGCGGATCCttaacgcacaattgcaata
BCO26_YhgD-F	ACATGCATGCatggaaacggaccgcaggct
BCO26_YhgD-R	CTAGTCTAGAtcagttctgcagcccttta
BCO26_1679-F	CTAGTCTAGAatgtctgttgcacaga
BCO26_1679-R	TCCCCCGGGttacaagccgcatttaatt
BCO26_RsbW-F	CGCGGATCCatggaggagttgtatcatat
BCO26_RsbW-R	CCGGAAATTCTcaggttggcagtttga
BCO26_YteA-F	CCCAAGCTTatgctgacaaaagaacaact
BCO26_YteA-R	CGCGGATCCtcattctttttctcg
BCO26_2825-F	CGCGGATCCatggggcgattcagatcat
BCO26_2825-R	CCGGAAATTCTtcatgcccggccccccctt
BCO26_LevE-F	CGCGGATCCatggcattggatatacggct
BCO26_LevE-R	CCGGAAATTCTtcatggatgaagcagtttat
BCO26_SigB-F	CGCGGATCCatgtcaaaactgcctcaacc
BCO26_SigB-R	CCGGAAATTCTctaattctccacatgttgca
BCO26_2573-F	ACATGCATGCatggaaaacattaaaatgct
BCO26_2573-R	CTAGTCTAGAtcaatgctttccccccta
BCO26_1484-F	CGCGGATCCatgaaacaaggtaaaagtaaa
BCO26_1484-R	CCGGAAATTCTtataatttcgaaacgttcg
pET28a-CspL-F	CATGCCATGGcaatgaaacatggcacagtaaa
pET28a-CspL-R	CCGCTCGAGttagtcttttgaacat
CspA-F	CGCGGATCCatgtccggtaaaatgactgg
CspA-R	CCGGAAATTCTttacaggctggttacgttac

pYES2-CspL-F	CGCGGATCC atggaacatggtacagtaaa
pYES2-CspL-R	CCGGAATTCTtagtctttttgaacat
pME6032-CspL-F	CCGGAATTCTtaggaacatggtacagtaaa
pME6032-CspL-R	CATGCCATGG tttagtctttttgaacat
77-cspL-F	CGGTTGGTAGGATCCACATATGGAGCACGGCA
77-cspL-R	CCGTGAAGT TATGACATGATTACGAATTCAAGTCCTCCTTCTG CACGTTGGCG

Supplementary Table 10. Sequences of oligonucleotide used in this study

RNA	Sequence (5' > 3')
RNA 1	CGGGAGAGGC GGUU UGCGUAUUGU
RNA 2	GGAGAGGC GGUU UGCGUAUUGU
RNA 3	GGGAGAGGC GGUU UGCGUAU
RNA 4	GGAGAGGC GGUU UGCGU
RNA 5	GCAUUA AUGAAU
RNA 6	GCAUUA AUGAA
RNA 7	CAUUA AUGAA
RNA 8	AUUA AUGAAU
RNA 9	AUUA AUGA
RNA 10	UAAUGA
RNA 11	UAAUG
RNA 12	AAUG
RNA 13	GAAUG
RNA 14	TAAUG
RNA 15	AAUGC
ssDNA 1	AGGTACCCGGGGATCCTCTAGAGTCGTC
ssDNA 2	TGTACCCGGGGATCCTCTAGAGTCGC
ssDNA 3	GTACCCGGGGATCCTCTAGAGTCG
ssDNA 4	GGGAGACC GGAAATT CGAGCTCG
ssDNA 5	GAGACC GGAAATT CGAGCT
ssDNA 6	GACC GGAAATT CGAG
ssDNA 7	CCGG AAATT CG
ssDNA 8	GGAATT
ssDNA 9	GAAT
ssDNA 10	GAATC
ssDNA 11	CGAAT
ssDNA 12	TGAAT

Supplementary Table 11. Synthetic gene sequences used in this study

Name	Sequence (5' > 3')
<i>cspL</i> -M11	ccatggca gaa cat ggt aca gta aaa tgg ttt aac agt gaa aaa gca gca gca gca gca gca gca gaa ggc gga gac gac gca gca gca ttc tcg gcc atc cag ggt gaa ggc tat aaa acg ctt gaa gaa ggc cag aaa gta tca ttt gat gtg gaa gaa gga tca cgc ggc ccg cag gcg gca aat gtt caa aaa gaa gac ctcgag
<i>cspL</i> -M7	ccatggca gaa cat ggt aca gta aaa tgg ttt aac agt gaa aaa gca gca gca gca gca gca gca gaa ggc gga gac gac gtg ttt gtc cat ttc tcg gcc atc cag ggt gaa ggc tat aaa acg ctt gaa gaa ggc cag aaa gta tca ttt gat gtg gaa gaa gga tca cgc ggc ccg cag gcg gca aat gtt caa aaa gaa gac ctcgag